## 'Delaval, Jan

From:

Roark, Jessica

Sent: To:

Wednesday, December 17, 2003 2:44 PM Delaval, Jan

Subject:

10/045180

Jan,

When things are up and running......

Please search, including pending, the following from 10/045180:

SEQ ID NO:3 against the DNA database SEQ ID NO:3 as an oligo against protein

SEQ ID NO:6 against DNA SEQ ID NO:6 as an oligo against protein

SEQ ID NO:4 against DNA SEQ ID NO:5 against DNA

Results on paper please.

Thanks!

Jessica H. Roark

CM1 8A03 Mailbox 9E12 Art Unit 1644 703 605-1209

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                 SUMMARIES
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HSCCSHP4
AF188268
AF184160
AF184159
AR270635
149588
HUMDFSNSIX
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RABNPCS4A
SS5S92
RABMCP2A
RABMCCS6A
S55578
RABDNP5A
AXS8765
RABDNP5A
RABDNP5A
RABDNP5A
RABDNP3AB
RABDNP3AB
RABNP3AB
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AX405718
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AF188269
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AR059558
AR063040
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BD074746
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BD074745
AF238378
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-MODEL=frame+ p2n.model -DEV=xlp
-Q=/Cogn2 1/05FPTO spool_p/USIO045180/runat 17122003 145023 12528/app query.fasta_1.860
-Q=/Cogn2 1/05FPTO spool_p/USIO1045180/runat 17122003 145023 12528/app query.fasta_1.860
-DB-GENEmbl -QFWR=fastap -SUPFIX=rge -MINMATCH=0.1_-LOOPCI=0 -LOOPEXT=0
-DNITS=bits -START=1 -END=-1 -MATRIX=blooun62 -TRRNS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=EXT -HEAPSIZE=500 -MINLEN=0 -MAXLEN=20000000000
-USER-USIO045180 @CCM 1 1 5283 @runat 17122003 145023 12528 -NCFU=6 -ICPU=3
-NO MMAP -LARGEQÜERY -NEG-SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRRADS=1 -XGRPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELEXT=7
                                                            December 17, 2003, 14:50:33; Search time 2689.5 Seconds (without alignments) 1429.821 Million cell updates/sec
                                                                                                                    94
                                                                                                 US-10-045-180A-3
514
1 MRILTLIASAFLLVALQAWAE.....GEHLGGTCFILGERYPICCY
         GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
                                            nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                              2888711 seqs, 20454813386 residues
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Perfect score:
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A99570 Sequence 1
BD07475 Human def
AF238978 Homo sapi
AC116559 Papio anu
AC138977 H.sapiens m
AF188159 Macaca mu
AF184150 Macaca mu
AF270635 Sequence 6
M98311 Homo sapien
M2130 Human meny
BD028213 Sequence 6
M25053 Human defen
A56051 Human defen
A56051 Human defen
A7405718 Sequence 4
M26602 Human defen
A71821 Human defen
A718220 Macaca mu
A2281 Human defen
A718220 Macaca mu
A2281 Human defen
A718229 Macaca mu
A2281 Human defen
A78621 Human defen
A78621 Human defen
A78621 Human defen
A78631 Human defen
A76602 Oryctolagus
A56883 Coryctolagus
A56883 Coryctolagus
A56883 Coryctolagus
A76884 Rabbit macr
L10842 Oryctolagus
A76886 Sequence
M64600 Oryctolagus
A7688765 Sequence
M64600 Oryctolagus
A76888 Rattus norv
U16688 Rattus norv

A98571 Sequence 2 BD074746 Human def

Description

AR355799 Homo sapi AR05958 Sequence AR053040 Sequence 193525 Sequence 46 AR059566 Sequence AR063048 Sequence

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61 LysGlyLeulleCysHisCysArgValLeuTyrCysIlePheGlyGluHisLeuGlyGly 80
JP 2001514264-A/2
11-SEP-2001
28-BVG-1999 JP 2000508701
LYDIE BOUGUELERET, ILYA SHAACOV
COTK14/435, A01N43/50, A01N63/00, A61K7/00, A61K38/00, A61P29/00, A61P35/00, A61P35/00, A61P35/00, A61P36/00, 
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unidentified
unidentified
unclassified.

1 (bases 1 to 4415)
Bougueleret,L. and Chumakov,I.
HUMAN DEFENSIN DEF-X, GENE AND DNAC, COMPOSITION CONTAINING SAME
AND DIAGNOSTIC AND THERAPEUTIC APPLICATIONS
PARENT: WO 9911663-A 1 11-MAR-1999;
BOUGUELERET LYDIE (FR); CHUMAKOV ILYA (FR)
                                                                                                                                                                                                                                                                                                                                                              containing the same, and application to diagnosis and remedy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 AspvalvalileTyrPheSerGlyAspAspSerCysSerLeuGlnValProGlySerThr
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Location/Qualifiers
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/mol type="genomic DNA"
/db_xref="taxon:9606"
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Sequence 1 from Patent W09911663.
A98570.
A98570.1 GI:6781626
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PN JP 2001514264-A/2
PD 11-5EP-2001
PR 28-AUG-1999 JP 2000
PR 29-AUG-1997 FR
PI LYDIE BOUGUELERET;
PC COTXA/435,A01N43/5
PC A61P35/00,
PC A61P35/00,
PC A61P35/00,
PC TSP21/02,CO7K16/18
C12P21/02,CO7K16/18
C12P21/03,CO7K16/18
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1 (bases 1 to 453)

Bougueleret, L. and Shmacov, I.

Human defensin polypeptide Def-x, genome DNA and cDNA, composition containing the same, and application to diagnosis and remedy
Patent: JP 2001514264-A 2 11-SEP-2001;
                                  PAT 26-JAN-2000
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Bougueleret,L. and Chumakov,I.
Bougueleret,L. and Chumakov,I.
HWAN DEFENSIN DEF.X, GENE AND DNAC, COMPOSITION CONTAINING SAME AND DIAGNOSTIC AND THEAPBUTIC APPLICATIONS
PARCH: WO 9911663-A 2 11.MAR-1999;
BOUGUELERET LYDIE (FR); CHUMAKOV LLYA (FR)
LOCATION/Qualifiers
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Sequence 2 from Patent WO9911663.
A98571
A98571.1 GI:6781627
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BD074746.1 GI:22620349
JP 2001514264-A/2.
Homo sapiens (human)
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PAT 26-JAN-2000

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 4415)
Bougueleret,L. and Shmacov,I.
Human defensin polypeptide Def-X, genome DNA and CDNA, composition containing the same, and application to diagnosis and remedy Patent: JP 2001514264-A I 11-SEP-2001;
                                                                                                                                                                                                                                                          BD074745

Human defensin polypeptide Def-X, genome DNA and cDNA, composition containing the same, and application to diagnosis and remedy
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JP 2001514264-A/1
11-SEP-2001
28-AUG-1998 JP 2000508701
29-AUG-1997 FR 97/10823
LYDIE BOUGUELERET, LLYA SHMACOV
COTKIL4/435,A01N43/50,A01N63/00,A61K7/00,A61K38/00,A61P29/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P35/00,A61P3/00,A6
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Human defensin polypeptide Def-X, genome DNA and cDNA,
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PN JP 2001514264-A/1

PN JP 2001514264-A/1

PD 11-SEP-2001

PF 28-AUG-1998 JP 2000508701

PR 28-AUG-1999 FR 97/10823

PI LYDIE BOUGUELERET,ILYA SHWACOV

PC GOYK14/A35,A01N43/50,A01N63/00,A61K3/00,A6

PC A61P37/02,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N1

C12P21/02,

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PC C12P21/02,

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CC TOPOLOGY: Linear;

CC Human defensin polypeptide Def-X, genome DNA and CDN
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db xref="taxon:966"
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BD074745.1 GI:22620348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3766 ATTCCAAGATATGACTGTGAAATTCACTAGATTTAAGATATAAGGAGATGCTACCTAGTT 3825
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
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This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (06-JUL-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany (bases 1 to 128544) Lagemann, D. and Platzer, M. Direct Submitsion Submitted (02-APR-2003) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany On Apr 2, 2003 this sequence version replaced gi:21700555.
                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (10-NOV-2000) Genome Analysis, Institute of Molecular
Biotechnology, Beutenberstr. 11, Jena 07745, Germany
5 (bases I to 128544)
Lagemann, D. and Platzer, M.
Direct Submission
                                                                                                                                                                                                                                                                                                              Submitted (24-MAY-2000) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany 4 (bases 1 to 12844) Genome Sequencing Center Jena.
                                                                                                                                                         Direct Submission
Submitted (12-FEB-2000) Genome Analysis, Institute of Molecular
Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
3 (bases 1 to 128544)
                     Unpublished

(bases 1 to 128544)
Schudte, B., Ganz, T., Linzmeier, R., Schudy, A., Schilhabel, M., Schutte, B., Ganz, T., Linzmeier, R., Ho.C.H., Hoang, B.V., McCray, P., Baumgart, C., Menzel, U., Schattevoy, R. and Rosenthal, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center clohe name: SCb-561b17
Sequencing vector: pUC18; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 127399 bases at least Q40
Consensus quality: 128330 bases at least Q30
Consensus quality: 12834 bases at least Q20
Quality coverage: 11.05x
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Center: Insitute of Molecular Biotechnology
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Contact: gscj-submit@genome.imb-jena.de
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  Chromosome 8 genomic sequence
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Homo sapiens chromosome 8 clone SCb-561b17 map p22-p21, complete
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  3586 TGCCAGCATGCAGAGCTACAGACTAGACAGAAGGACAGGAGACAGGCTCTGGAATTGGAT 3645
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (Dases 1 to 128544)
Polley,A., Baumgart,C., Blechschmidt,K., Dette,M.D., Jahn,N., Menzel,U., Reichwald,K., Schilhabel,M.B., Schudy,A., Taudien,S., Wen,G., Schutte,B., Malik,M., Peng,J.Hong., McCray,P. and Rosenthal,A.
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44435 a 36508 c 35861 g 46065 t 224 others
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* consists of 3 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* 6316 6415; gap of unknown length
* 6316 16704; contig of 6315 bp in length
* 16705 16804; gap of unknown length
* 16705 16804; gap of unknown length
* 16705 16804; gap of unknown length
* 16805 16303; contig of 146289 bp in length.
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/organism="Papio anubis"
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Papio anubis clone rp41-339c10, WORKING DRAFT SEQUENCE, 3 ordered
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(bases 1 to 163093)

Xu,W., Hua,A., Edhler,E. and Roe,B.A.

Direct Submission

Submitted (29-MAR-2002) Department Of Chemistry And Biochemistry,

The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,

OK 73019, USA

(bases 1 to 163093)

Xu,W., Hua,A., Elchler,E. and Roe,B.A.

Direct Submission

Submitted (30-MAY-2003) Department Of Chemistry And Biochemistry,

The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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1 (bases 1 to 163093)

Xu, W., Hua, A., Eichler, E. and Roe, B.A.

Papio, anubis BAC Clone rp41-339c10
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/clone_lib="RPCI - 41 Male (Olive) Baboon BAC Library" BASE COUNT 53384 a 41769 c 40796 g 52555 t 100 others ORIGIN	Alignment Scores: 2.05e-25 Length: 188604 Pred. No.: 300.00 Matches: 79 Score: 300.00 Matches: 3 Best Local Similarity: 27.62% Mismatches: 9 Query Match: 58.37% Indels: 195 DB: 2 Gaps: 1	US-10-045-180A-3 (1-94) x AC116558 (1-188604)	Qy         4 LeuThrLeuleuSerAlaPheLeuleuValAlaleuGlnAlaTrpAlaGluProLeuGln 23	24 AlaargalaHisGluMetProAlaGlnLysGlnProProAlaAspAspGlnAspValVal 43	Db 142597 GCAAGAGCTGATGAGATGCCCAGGAGCAGCCTCCAGCAAACGACCAAGATGTGGTC 142538	Oy 44 IleTyrPheSerGlyAspAspSerCysSerLeuGlnVal		Db 142477 GAAGAGCTACAGACTAGAGGAAGGAACGGGAGACAGGCTCTGGAATTGGGTCTCAGTGGT 142418	9556 yy	Db 142417 ACATGTCACTTAGGTGGCTTTACTTAACATCTCTGGTTGTTCTCATGTCTAAAT 142358	Qy 56 56	Db 142357 GGGATAGAGAACCAAATAAATCTAAGAGATTTTTCTTTCCCAAAAACATGATTCCAAGA 142298	95 56 YQ	Db 142297 TAIGACTGAAATTCACTAGGTTTAAGATATAAGGAGATGCTACCTAGTTCCTTCTGGATC 142238	δς	Db 142237 CAGACAAATAAGCTTAAGTATATAGAAAATATTTCACCGTGTCTATGTAGGAGGTTTTAG 142178	93 29 Kö	Db 142177 AACCTGGAGAGCCTAAGAGTGTGTTCAAGTGTGTGTGTGT	Qy 56 56	AAAGTGAAGCCAAGGAGAATGAGTCTCGAGTCCTGTGTGACCAGCACTGCTCTGTGTATT	Qy 56 56 Y	Db 142057 TATTCCTATTGACTGAGATTGTTTCTGCTACCGGCTGCAATACAGCCAACATCACTCATC 141998	95 56 YQ	Db 141997 AGTCAACAGGTGACTTCTCCCAAGATTCCCTTTACCATCCACTGCGGACCCCATACTGAAT 141938	Oy 57	Db 141937 TTCTGATGCTCTCTGGTTCCCCAGGCTCAACGAAGGGCTTGAGCTGCCATTGCAGAT 141878	69	141877 ACTCTACTGCCTTTTTG	89 rProlleCysCysTyr	DD 141817 CCCAAFCTGCTGCTAC 141802
Qy 56 56 Db 33475 TATTCCTATTGACTGAGATTGTTTCTGCTACCGGCTGCAATACAGCCAACATCACTCATC 33534	Qy         56	Qy 69 LeuTyrCysIlePheGlyGluHisLeuGlyGlyThrCysPheIleLeuGlyGluArgTy 89	Db 33655 ACTCTACTGCCTTTTTGGAGAACATCTTGGTGGGACCTCCTTCATCCATGGTGAACGCTC 33714 Ov 89 rProlleCvsTvr 94	Db 33715 CCCAATCTGCTGCTAC 33730	RESULT 7	LOCUS LOCUS DEFINITION Papio anubis clone rp41-273g19, WORKING DRAFT SEQUENCE, 2 ordered	ACCESSION AC11655816 GI:30725961 VERSION AC11655816 GI:30725961 VERSION AC11655816 GI:3077	Ş			REFERENCE I (Dasses I to Issout) THORNS XU,W., Hua,A., Eichler,B. and Roe,B.A. THIRD PARTY DATE TO PARTY DATE.		REFERENCE 2 (bases 1 to 188604) AUTHORS Xu,W., Hus, A., Eichler,E. and Roe,B.A.	AL	OK 73019, USA (1986AA)	TITIES XI,W., Hua,A., Eichler,E. and Roe,B.A.		1.28173120	On May 13, 2003 this sequence version	Center: Department of Chemissiry And Brochemissiry The University Of Oklahoma Center code:UOXXXXX	to the second of	* NOIS: Inly is a "Working Grait" Sequence. It currently * Consists of 2 contigs. Gaps between the contigs. * are represented as thing of M. The order of the nieps	* is believed to be correct as given, however the size s * of the gard hetween them are given or estimates that have	* provided by the submitter.	* ints Sequence Will be replaced * by the finished sequence as some it is available and * the archaedon number will be preserved	* 6058 * 6057. can of under length	* 6158 188604: Contig of 182447 bp in length. FEATURES Location/Qualifiers	source 1188604 /organism="Papio anubis"	/mol_type="genomic DNA" /db_xref="taxon:9555"	/clone="rp41-273g19"

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                                                                                          231
112 CCACTCCAGGCCAAGAGGTGATGAGGCTCCAGGCCAGGAGCAGCGTGGGCCCAGAAGACCAG 171
                                                                                                                                                                                            232 AGGGGCATGGTCTGCTCTTGCAGATTAGTATTCTGCCGGCGAACAGAACTTCGTGTTGGG 291
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Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
                                                                        172 GACATATCTATTTCCTTTGCATGGGATAAAAGCTCTGCTCTTCAGGTTTCAGGCTCAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 347)
Tang, 'Zo, Yuan,'Jo, Miller, C.J. and Selsted, M.E.
Isolation, characterization, cDNA cloning, and antimicrobial properties of two distinct subfamilies of alpha-defensins from
                                                                                                                                            41 AspValValileTyrPheSerGlyAspAspSerCysSerLeuGlnValProGlySerThr
                                                                                                                                                                                                                                                                                                                                                                                     AF188268 347 bp mRNA linear Macaca mulatta defensin-1 mRNA, complete cds. AF188268
                                                                                                                                                                                                                                                                                 292 AACTGCCTCATTGGTGTGTGTGTTTCACATACTGCTGC 330
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Mismatches:
Indels:
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Infect. Immun. 67 (11), 6139-6144 (1999)
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Selsted, M.E.
Rhesus myeloid defensins
Unpublished
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Selsted, M.E.
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SFAWDKSSALQVSGSTRGMVCSCRLVFCRRTELRVGNCLIGGVSFTYCCTRVD"
                                                                        PRI 07-JUN-1999
                                                                                                                                                                                                                                                                                                                                                contains a
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1 (Dases 1 to 52)

Palfree, R.G., Sadro, L.C. and Solomon, S.

The gene encoding the human corticostatin HP-4 precursor contains recent 86-base duplication and is located on chromosome 8 Mol. Endocrinol. 7 (2), 199-205 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (05-MAY-1992) R.G.E. Palfree, McGill University Royal
Victoria Hosp., Rm L2.05, 687 Pine Ave West, Montreal PQ, H3A 1A1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="recent duplication of immediate upstream segment" 137 c 135 g 152 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue type="bone marrow"
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/product=="corticostatin/defensin HP-4 precursor"
/protein_id="CAA46792.1"
/db_xref="GI:29735"
                                                                        linear
                                                              הפרוב האזה קל 42 bp mRNA linea
H.sapiens mRNA for corticostatin HP-4 precursor.
X65977
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330. .412
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/organism="Homo sapiens"
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                                                                                                                                         X65977.1 GI:29734
corticostatin/defensin.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="HP-4"
109. 342
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Palfree, R.G.E.
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mRNA linear PRI 14-NOV-1999 (MNP1) mRNA, complete cds.
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Macaca mulatta
Makaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
Thasas i to 43.3
Zhao, C., Nguyen, T. and Lehrer, R.I.
cDNA cloning of three alpha-defensins and three demidefensins from Unpublished
2 (bases 1 to 433)
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               57
                                                                             58 GlySerThrLysGlyLeuIleCysHisCysArgValLeuTyrCysIlePheGlyGluHis 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhao, C., Nguyen, T. and Lehrer, R.I.
Direct Submission
Submitted (10-SEP-1999) Medicine, UCLA, 10833 Le Conte Avenue,
Angeles, CA 90095, USA
            40 GlnAspValVallleTyrPheSerGlyAspAspSerCysSerLeuGln-----ValPro
                                                                                                                                                                 253 CGCTATGGAACCTGCTTCTACCTGGGAAGAGTCTGGGGCATTCTGCTGC 300
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Conservative:
Mismatches:
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/mol_type="mRNA"
/db_xref="taxon:9544"
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Macaca mulatta alpha-defensin 1
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/protein_id="AAP07926.1"
/bx.ref="61:6409290"
/tanslation="MRTLAILAVALQAQAEPLQARTDEATAAQEQIPTDNPEVV
VSLAMDESLAPKDSYPCLRKINMACYCRIPACLAGERRYGTCFYLGRVWAFCC"
113 c 104 g 98 t
                                                                                                                                                                                                                                                                                             AF184160 435 bp mRNA linear PRI 14-NOV-1999
Macaca mulatta alpha-defensin 1A (MNP1A) mRNA, complete cds.
AF184160
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(basea I to 435)

Zhao, C., Nguyen, T. and Lehrer, R.I.

cDNA cloning of three alpha-defensins and three demidefensins from
                                                                                172 CCAGAAGTGGTTGTTTCCCTTGCTGGGATGAAAGCTTGGCTCCAAAGGATTCAGTCCCA 231
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                                                               57
                                                                                                                             GlySerThrLysGlyLeulleCysHisCysArgValLeuTyrCysIlePheGlyGluHis 77
ProLeuGlnAlaArgAlaHisGlu---MetProAlaGlnLysGlnProProAlaAspAsp 39
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                                                             40 GlnAspyalyalıleTyrPheSerGlyAspAspSerCysSerLeuGln-----yalPro
                                                                                                                                                                                                                             292 cecrardeaaccrecricraccredeaagagrergescarrerecred 339
                                                                                                                                                                                            78 LeuGlyGlyThrCysPhelleLeuGlyGluArgTyrProlleCysCys 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (10-SEP-1999) Medicine, UCLA, 10833 Le Angeles, CA 90095, USA
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Matches:
Conservative:
Mismatches:
Indels:
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/mol_type="mRNA"
/db_xref="taxon:9544"
1. 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
2 (bases 1 to 435)
Zhao,C., Nguyen,T. and Lehrer,R.I.
Direct Submission
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/codon_start=1
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Best Local Similarity:
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/processin id="AABE59357.1"
/bd xref="G1:181547.1"
/db xref="G1:181547.1"
/translerion="WRTITILTAVILIVALQAKAEFLQAEDDFLQAKAYEADAQEGRGA NDQDFAVSFAEDASSSLRALGSTRAFTCHCRRSCYSTEYSYGTCTVMGINHRFCCL" 319. .440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (Dases 1 to 452)
Jones, D.E. and Bevins, C.L.
Jones, D.E. and Bevins, C.L.
antimicrobial peptides in host defense of the human bowel
PEBS Lett. 315 (2), 187-192 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 GlnProProAlaAspAspGlnAspValValIleTyrPheSerGlyAspAspSerCysSer 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 LeuGlnValProGlySerThrLysGlyLeuIleCysHisCysArgValLeuTyrCysIle 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source text: Homo sapiens small intestine cDNA to mRNA.
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Conservative:
Mismatches:
Indels:
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production and use thereof
Patent: US 5641497.A 6 24-UUN-1997;
Location/Qualifiers
1. .452
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/mol_type="mRNA"
/db xref="taxon:9606"
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'codon_start=1
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                                                                                                  /organism="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 452)
Au-Young, J. and Seilhamer, J.J.
Composition for the detection of signaling pathway gene expression
Patent: US 650038-A 1198 31-DEC-2002;
Location/Qualifiers
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|TTAGAGCTTTGGGCTCAACAAGGGCTTTCACTTGCCATTGCAGA---AGGTCCTGTTAT 255
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  133 CCAGAAGTGGTTGTTTCCCTTGCCTGGGATGAAAGCTTGGCTCCAAAGGATTCAGTCCCA 192
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                                                 58 GlySerThriysGlyLeuIleCysHisCysArgValLeuTyrCysIlePheGlyGluHis 77
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Bevins,C.L. and Jones,D.E.
Gastrointestinal defensins, cDNA sequences and method for the
                                                                                                                                                                            253 CGCTATGGAACCTGCTTCTACATGGGAAGAGTCTGGGCATTCTGCTGC 300
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07-NOV-1994
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CDNA to computer-readable sequence [1] kindly submitted by K.Daher, 25-NOV-1988.

Submission form for [1] kindly provided by M.Kronenberg,
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1 (Assas 1 to 448)
Daher, K.A., Lehrer, R.I., Ganz, T. and Kronenberg, M.
Isolation and characterization of human defensin cDNA clones Proc. Natl. Acad. Sci. U.S.A. 85 (19), 7327-7331 (1988)
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VERSION
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SOURCE
ORGANISM
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BX099382
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                                                                                                                                                    No.
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-MODEL=frame+ p2n.model -DEV=xlp
-O=/Cgn2 1/USFYO spool p/USION05580/runat 17122003 145024 12540/app_query.fasta_1.860
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-USER-SIG0045180 @GGN 1 1.6100 @runat 17122003 145024 12540 -NCPU=6 -ICFU=3
-NO MMAP -LARGEQUERY -NGG SCORES=0 -MAIT -DSPBLOXE=10 -LOUGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                2003, 14:50:33 ; Search time 3286.5 Seconds (without alignments) 695.153 Million cell updates/sec
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                                                                                                                                                                                                                       1 MRTLTLLSAFLLVALQAWAE......GEHLGGTCFILGERYPICCY
                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                    OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                             22781392 segs, 12152238056 residues
                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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gb_gssl:*
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                                                                                                                    December 17,
                                                                                                                                                                                                                                                      BLOSUM62
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Perfect score:
                                                                                                                                                                                                                                                        Scoring table:
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database
                                                                                                                       on:
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N

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/dev stage="Adult"
// lab_host="DHIOB (Life Technologies)"
// clone lib="DHIOB (Life Technologies)"
// clone lib="DHIOB (Life Technologies)"
// clone lib="DHIOB (Life Technologies)"
// note="Organ: Bone; Vector: pT/T3-Pac (Pharmacia) with a modified polylinker; Site_1: BcoR I; Site_2: Not I;
NCI_CGAP_DPO is a cDNA library containing the following tissue (8): Subchondral Bone. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996, First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT/T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (TT) 18 tail. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=Yes.
                                                                               634 bp mRNA linear EST 23-SEP-2002
NCI_CGAP_DF0 Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  509 ATGAGGATTATCGCCCTCCTCGCTGCTATTCTCTTGGTAGCCCTCCAGGTCCGGGCAGGC 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAlaGlu 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 ProLeuglnAlaArgAlaHisGluMetProAlaGlnLysGlnProProAlaAspAspGln 40
                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 634)

                                                                                                                                                                                                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence tag for this library is GTTAAGCGTC.
TAG LIB-UI-H-DFO
TAG TISSUE=subchondral bone
TAG SEQ-GTTAAGCGTC"
TAG SEQ-GTTAAGCGTC"
TAG SEQ-GTTAAGCGTC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     634
146
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/mol_type="mRNA"
/mol_traxon:9606"
/clone="UI-H-DF0-ben-n-14-0-UI"
                                                                                                     UI-H-DF0-ben-n-14-0-UI.si NCI CGAP DF0 HC
UI-H-DF0-ben-n-14-0-UI 3', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissue_type="Subchondral Bone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cocation/Qualifiers
                                                                                                                                                                               BU616655.1 GI:23282870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.38e-15
227.00
64.52%
                                                                                                                                                                                                                                 Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49.46% 44.16%
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                                                                                                                                                          BU616655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                          RESULT 2
BUG16655/c
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                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                              AUTHORS
TITLE
                                                                                                                                                          ACCESSION
                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
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/lab host="mbH10B"
/clone="lorgan: mixed (see below); Vector: pT7T3D-Pac
/parmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHW, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 250232-265223,
340488-34549, and 484488-489479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 GACATATCTTTGCATGGGATAAAGCTCTGCTCTTCAGGTTTCAGGCTCAACA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 ATGAGGATTATCGCCCTCCTCGCTGCTATTCTCTTGGTAGCCCTCCAGGTCCGGGCAGGC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCACTCCAGGCAAGAGGTGATGAGGCTCCAGGCCAGGAGGCGTGGGCCAGGAAGACCAGG
                                                                                                                                                                                                                                                                                                                                                                                                 www.rzpd.de
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seg primer:
Ml3r, Primer Sequence: TTTCACACAGGAAACAGCTATGAC.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAlaGlu 20
Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
Radelof,U., Schneider,D. and Korn,B.
Human UnigeneSet - RZPD3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AspValValIleTyrPheSerGlyAspAspSerCysSerLeuGlnValProGlySerThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LysGlyLeulleCysHisCysArgValLeuTyrCysIlePheGlyGluHisLeuGlyGly
                                                                                             Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD: INAGP998H14549.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-
bin/show.lip.pl.cgl/response7libNo-972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: 449 30 32639 101
Fax: 449 30 32639 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  310 AACTGCCTCATTGGTGTGTGTTTCACATACTGCTGC 348
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 370)
10 is Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Eriones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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/dob_stage="Adult"
/clone lib="Adult"
/clone lib="mrol129"
/note="Organ: marrow, Vector: pucl8; Site_1: Smal; Site_2:
Smal; A mini-library was made by cloning products derived
from ORESTES PRC (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
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Email: asimpsonaludwig.org.br
This asimpsonaludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3&t2=QV3-MT0129-
111100-427-901kt3=22000-11-11&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 370.
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QV3-MI0129-111100-427-g01 MT0129 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                   191 CCAGAAGTGGTTGTTTCCCTTGCATGGACGAAAGCTCGGCTCCAAAGCTCCAGGGTCA 132
                                                                                                                                                                        311 ATGAGGACCCTCGCCATCCTTGCTGCCATTCTCTCGTGGCCCTGCAGGCCCAGGCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 AGGAAAAACATGGCCTGCTATTGCAGAATACCAGCGTGCATTGCAGGAGAACGTCGCTAT 72
                                                                                                                      1 MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAlaGlu 20
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAACCTGCATCTACCAGGAAGACTCTGGGCATTCTGCTGC 30
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//db xref="taxon:9606"
/dev_stage="Adult"
/doone lib="Mr0343"
//orde="Organ: marrow; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORBSTES PCR (U.S. Letters Patent application No. 196; 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 349)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Brunstein,A., deoliveira,P.S., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-MT0343-
170101-665-a05&t3=2001-01-17&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 349.
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CM3-MT0343-170101-665-a05 MT0343 Homo sapiens CDNA, mRNA sequence.
                                                                             329 AGGGGCATGGTCTGCTCTTGCAGATTAGTATTCTGCCGGCGAACAGAACTTCGTGTGGG 270
CCACTCCAGGCAAGAGGTGATGAGGCTCCAGGCCCAGGAGCAGGGCGTGGGCCAGAAGACCAG 390
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                                                                                                61 LysGlyLeulleCysHisCysArgValLeuTyrCysllePheGlyGluHisLeuGlyGly
                                              41 AspValValIleTyrPheSerGlyAspAspSerCysSerLeuGlnValProGlySerThr
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Email: asimpson@ludwig.org.br
This asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3&t2=QV3-MT0129-
Ill100-427-c03&ta=2000-11-11&t4=1)
Seg primer: pug 18 forward
High quality sequence stop: 372.
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QV3-MT0129-111100-427-c03 MT0129 Homo sapiens CDNA, mRNA sequence.
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I bases I to 37.2

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Marcuskuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 CCAGAAGIGGTIGTITCCCTIGCACGAGGACGAAAGCTIGGCTCCAAAGCATCCAGGCTCA 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87 ATGAGGACCCTCGCCATCTTGCTGCTATCTCCTGGTGGCCCTGCAGGCCCAGGCTGAG 146
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into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
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Matches:
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KEYWORDS
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AUTHORS
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                                                                           ORIGIN
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SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
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Homo sapiens cDNA, mRNA
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265 AGGAAGAACATGGCCTGCTATTGCAGAATACCAGCGTGCATTGCAGGAGAAACGTCGCTAT 324
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1-3, Yanada-oka, Suita, Osaka Pref. 565, Japan
1-1, Yanada-oka, Suita, Osaka Pref. 565, Japan
1-1: 06-877-5111(ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DDBJ
Since 1993. For the abundance information of clones with this
sequence in this library and as well as in other 3'-directed
libraries, see 'http://www.imcb.osaka- u.ac.jp/bodymap'. The
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Matches:
Conservative:
Mismatches:
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Institute for Molecular and Cellular Biol
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HUMGS0008342 Human adult (K.Okubo)
                             l. .372
/organism="Homo sapiens"
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Homo sapiens (human)
Homo sapiens
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Mammalia; Eutheria;
1 (bases 1 to 379)
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/note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196; 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
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Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa, Chordata; Craniata; Vertebrata; Eutheria;
1 (bases 1 to 389)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Nagai,M.A., da Silva,W. Jr., Ratenkuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
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СМЗ-МТО343-170101-666-£02 МТО343 Ноmo sapiens cDNA, mRNA sequence.
BI021710
                Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br.scripts/gethtml2.pl?tl=RC5&t2=RC5-MT0259-170101-011-B02&t3=2001-01-17&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 387.

1. .387
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1. (Dases 1 to 387)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveire,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
sequences of the clones represented by this GS sequences is also found there.
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/note="One or more human adult tissue"
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JOURNAL MEDLINE PUBMED

COMMENT

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/mol type="mRNA"
/db xref="taxon:9606"
/dev stage="Adult"
/clone lib="wrf012"
/note="Organ: marrow; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 ,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pax: +55-11-2704922

Pax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3&t2=QV3-MT0129-111100-419-d01&t3=2000-11-11&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 38

High quality sequence stop: 396.
                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 396)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvahlo, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveire, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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                                                                                                                                                                                                                                                                                                                                                                        Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
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/organism="Homo sapiens"
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/mol type="mmna" "mon type="mmna" "mol type="mmna" "mol type="mmna" "mol type="mmna" "mole="mole lib="mylola" "marrow; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ONESTES POR (U.S. Letters Patent application No. 196; 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
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                                                                                                                                                                                   Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-MT0343-170101-666-f02&t3=2001-01-17&t4=1)
Seq primer: puc la forward
High quality sequence start: 52
High quality sequence stop: 389.
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                                                                                             Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAlaGlu
                        97 (7), 3491-3496 (2000)
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quality sequence stop: 389.
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/note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196
/716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue mkNA and cDNA amplification were performed under low
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1 (bases 1 to Accia Correa, R., Verjovski-Almeida, S., Briones, M.R., Sogai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matenkuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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QV3-MT0129-111100-426-c04 MT0129 Homo sapiens cDNA, mRNA sequence.
BF893435
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Fax: +55-11-2707001

Bmail: asimpsom@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3&t2=QV3-MT0129-11100-42&e-co4&t3=2000-11-11&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 419.
                  60 ThriysGlyLeuIleCysHisCysArgValLeuTyrCysIlePheGlyGluHisLeuGly 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                165 GGAACCTGCATCTACCAGGAAGACTCTGGGCATTCTGCTGC 124
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                                                                           GlyThrCysPhelleLeuGlyGluArgTyrProlleCysCys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nlb.gov
Tissue Procurement: Elisabeth Paietta, Jonathan D. Licht, M.D.,
Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco.
                                                                                                                               AW468012 413 bp mRNA linear EST 24-FEB-2000 he30d11.x1 NCI CGAP CML1 Homo sapiens cDNA clone IMAGE:2920533 3' similar to gb:M26602 NEUTROPHIL DEFENSINS 1, 2 AND 3 PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCACTCCAGGCAAGAGTGATGAGGTTGCTGCAGCCCCGGAGCAGATTGCAGCGGACATC 286
                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mamaalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (Dases 1 to 413)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Gancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAlaGlu 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 GGAACCTGCATCTACCAGGGAAGACTCTGGGCATTCTGCTGC 113
                93
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            GlyThrCysPhelleLeuGlyGluArgTyrProlleCysCys
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Matches:
Conservative:
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                   AW468012.1 GI:7038118
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218.50
64.89%
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Pred. No.:
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DB:
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                                                                                         RESULT 10
AW468012/c
                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 424)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       424 bp mRNA linear EST 18-JAN-2001
QV3-MT0129-111100-419-h09 MT0129 Homo sapiens cDNA, mRNA sequence.
BF893232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the PAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3&t2=QV3-MT0129-
111100-419-h09&t3=2000-11-11&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 21
High quality sequence stop: 424.

Location/Qualifiers
                                                                                                                                                                                                                                                                                           233 AGGAAAAACATGGCCTGCTATTGCAGAATACCAGCGTGCATTGCAGGAGAAACGTCGCTAT 174
293 CCAGAAGTGGTTGCTTGCTTGCATGGGACGAAAGCTTGGCTCCAAAGCATCCAGGCTCA 234
                                                                                                                      353 CCACTCCAGGCAAGAGCTGATGAGGTTGCTGCAGCCCCGGAGCAGATTGCAGCGGACATC 294
                                                                                                                                                                  40 GlnAspvalvalleTyrPheSerGlyAspAspSerCysSerLeuGlnValProGlySer 59
                                                                                                                                                                                                                                                                   60 ThrLysGlyLeulleCysHisCysArgValLeuTyrCysIlePheGlyGluHisLeuGly 79
                                                                            ProLeuGlnAlaArgAlaHisGluMet---ProAlaGlnLysGlnProProAlaAspAsp 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                   173 GGAACCIGCAICTACCAGGGAAGACTCIGGGCAITCIGCIGC 132
                                                                                                                                                                                                                                                                                                                                                            80 GlyThrCysPhelleLeuGlyGluArgTyrProlleCysCys 93
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/organism="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
/dev_stage="Adult"
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clone lib="MT0129"
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Fax: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3&t2=QV3-MT0129-11100-419-hO3&t3=2000-11-11&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 23
High quality sequence stop: 425.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases I to 425)

1 (Dases I to 425)

1 (Dases I to 425)

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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                                                                                                                                                                                                                                   mRNA sequence.
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          425 bp mRNA linear
QV3-MT0129-111100-419-h03 MT0129 Homo sapiens CDNA,
BF893231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 GGAACCTGCATCTACCAGGAAGACTCTGGGCATTCTGCTGC 102
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                 454
474
324
132
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Mismatches:
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/organism="Homo sapiens"
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Ludwig Institute for Cancer Re
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               1,72e-14
218.50
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Homo sapiens
                                                                                    Best Local Similarity:
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                                                            Percent Similarity:
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/clone libe soares NFL T GBC_SI"
//clone libe Soares NFL T GBC_SI"
//note= "Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHil9W, testis NHT, and B-cell
NCI_CGAP_GCBI) were mixed, and se clicles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "
00 a 106 c 115 g 109 t
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wf36d08.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone
IMAGE:2357679 3' Similar to gb:M26602 NEUTROPHIL DEFENSINS 1, 2 AND
3 PRECIRSOR (HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              284 CCAGAAGTGGTTGTTTCCCTTGCATGGGACGAAGCTTGGCTCCAAAGCATCCAGGCTCA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAlaGlu 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mamaalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 430)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 286 Std Error: 0.00 Seq primer: -4UVP from Gibco.
Location/Qualifiers
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                                                       /note="Organ: marrow; Vector: pucl8; Site 1: Smal; Site 2: Smal; A mini-library was made by cloning products derived from ORESTES FOR (U.S. Letters Pattent application No. 196, 716 - Ludwig Institute for Cancer Research) profiles into the DUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low a stringency conditions.
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430 bp mRNA linear BST 07-MAR-2000 wa72b06.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone IMAGE:2301683 3' Similar to gb:M26602 NEUTROPHIL DEFENSINS 1, 2 AND 3 PRECTRSOR (HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 CCAGAAGTGGTTGTTTCCCTTGCATGGACGAAAGCTTGGCTCCAAAGCATCCAGGCTCA 208
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NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 526 Std Error: 0.00 Seq primer: -400P from Gibco.
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/dev_stage="Adult"
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/ Organism="Homo sapiens"
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Search completed: December 17, 2003, 18:25:42 Job time : 3291.5 secs

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cytostatic; anticancer; inflammation; tissue repair;
endocrine regulation; corticostatic regulation; cancer; melanoma;
AIDS; immune deficiency; psoriasis; ss.
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-MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgn1 /USPSTO spool p/USR.0045180/runat 17122003 145023 12520/app query.fasta_1.860
-DB=N denseeq 195un03 -QFWR=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MARRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -UOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NOFM=ext -HEAPSIZE=500 -MINLENE=0 -MAXLEN=200000000
-USER=USIO045180 @CGN 1 835 @runat 17122003 145023 12520 -NCFU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOPE -DELEXT=7
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1 MRTLTLLSAFLLVALQAWAE......GEHLGGTCFILGERYPICCY
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                                                                                                           OM protein - nucleic search, using frame_plus_p2n model
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Copyright (c) 1993
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AAX26698 standard; cDNA; 453
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    useful as antimicrobial agent,

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                                                                          97FR-0010823
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polypeptide can be used as an antimicrobial, antiparasitic agent or a pesticide. The Def-X polypeptide can be used as a cytostatic agent or especially anticancer) agent, and as an agent for modulating processes of inflammation, tissue repair and endocrine (especially corticostatic) regulation. The polypeptide can be used in a composition for external topical use, especially in a cosmetic composition. Compositions of microbial containing Def-X can be used for prevention and treatment of microbial and parasitic infections, especially where the microbial or parasitic infections or negative bacterial infections or mycobacterial, fungal or spirochaete infections, or where the viral infections are associated with enveloped viruses, especially HSV and HIV.

The compositions can used for prevention and/or treatment of cancer, especially melanomas, or liver cancer, prostate cancer, non-small-cell lung cancer or colorectal carcinoma, and for chhancing immunity, especially in the treatment of postiasis, as well as for modulating inference. Inflammatory processes, especially in the case of AIDS, or preventing immune deficiency, is inflammatory processes, especially in the case of AIDS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes human defensin (Def-X). The Def-X
                                                                                                   cDNA sequence encoding human defensin (Def-X) protein.
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The present sequence encodes human defensin (Def-X). The Def-X polypeptide can be used as an antimicrobial, antiparasitic agent or a pesticide. The Def-X polypeptide can be used as a cytostatic cast of especially anticancer) agent, and as an agent for modulating processes of inflammation, tissue repair and endocrine (especially corticostatic) regulation. The polypeptide can be used in a composition for external topical use, especially in a cosmetic composition. Compositions containing Def-X can be used for prevention and treatment of microbial cand parasitic infections are Gram-positive or -negative bacterial infections or mycobacterial, fungal or spirochaete infections, or where the viral infections are associated with enveloped viruses, especially HSV and HIV. The compositions can used for prevention and/or treatment of cancers, infections are colorectal carcinoma, and for enhancing immunity, especially in the crase of AIDS, or preventing immune deficiency, especially in the treatment of posciaes, as well as for modulating inflammatory processes, especially in the case of AIDS.
                                                              172 GAIGTGGTCATTTACTTTTCAGGAGATGACAGCTGCTCTTCAGGTTCCAGGCTCAACA 231
                                                                                                                     112 CCGCTCCAGGCAAGAGCTCATGAGATGCCAGCCCAGAAGCAGCCTCCAGCAGATGACCAG 171
                                                                                                 LysGlyLeulleCysHisCysArgValLeuTyrCysllePheGlyGluHisLeuGlyGly
                               41 AspvalvalileTyrPheSerGlyAspAspSerCysSerLeuGlnValProGlySerThr
                                                                                                                                                                                                                                                                                                                                                                                                       Human defensin; Def-X; antimicrobial; antiparasitic; pesticide; cytostatic; anticancer; inflammation; tissue repair; endocrine regulation; corticostatic regulation; cancer; melanoma; AIDS; immune deficiency; psoriasis; ss.
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                                                                                                                                                                ThrcysPheileLeuGlyGluArgTyrProileCysCysTyr 94
                                                                                                                                                                                                                                                                                                                                                                        Nucleotide sequence of human defensin (Def-X),
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Alignment Scores:

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                                                                                                                                                                        ProLeuGlnAlaArgAlaHisGluMetProAlaGlnLysGlnProProAlaAspAspGln
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                            Conservative:
Mismatches:
Indels:
     Length:
Matches:
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                                                                     Gaps:
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                                                                                           US-10-045-180A-3 (1-94) x AAX26696
8.7e-38
393.50
32.41%
32.41%
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Best Local Similarity:
Query Match:
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Indels:

44.16%

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This invention relates to a combination comprising several cDNAs that are differentially expressed in activated vascular tissue. The invention are differentially expressed in activated vascular tissue. The invention care also discloses a high throughput method for detecting differentially expressed cDNAs in a sample. The cDNAs of the invention may have antidiabetic; gynaecologically vasotropic and cerebroprotective activities and may be used in gene therapy. The cDNAs of the invention may be used in a mapple, or compound that specifically binds a cDNA of the invention. A protein encoded by the cDNA may be used to screen several cidentify a molecules or compounds to identify a nationally binds a cDNA of the protein, or to produce or purify an antibody to the protein that can be used to detect a protein in a sample or purify a natural or recombinant protein from a sample. The nucleotides may be useful for diagnosing, stading, treating, or monitoring the progression of treatment of a vascular disease, e.g. atherosclerosis, cancer, cornary creptings injury, restenosis, or stroke. The cDNAs can also be used to also injury, restenosis, or stroke. The cDNAs can also be used con algebratesion injury, restenosis, or stroke. The cDNAs can also be used con algebratesion injury, restenosis, or stroke. The cDNAs can also be used con an order a discoules. Antibodies to the proteins encoded by the cDNAs are useful for diagnosing pre-pathologic disorders, and chronic mount or distribution of the profession.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Combination for diagnosing, staging, treating, or monitoring the progression of treatment of a vascular disease, e.g. atherosclerosis, comprises several cDNAs that are differentially expressed in activated vascular tissue.
                                                                              Human cDNA #473 differentially expressed in activated vascular tissue.
                                                                                                                     Human; gene; ss; vascular tissue; cytostatic; atherosclerosis; cardiant; hypotensive; antidiabetic; gynaecological; vasotropic; cerebroprotective; gene therapy; vascular disease; cancer; coronary; artery disease; hypertension; diabetes; pre-eclampsia; restenosis;
                                                                                                                                                                                                          ischaemia-reperfusion injury; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page -; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                     08-JAN-2002; 2002US-0044090.
                                                                                                                                                                                                                                                                                                                                                                                                            28-JUL-2000; 2000US-222469P.
                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BAND/) BANDMAN O.
                                                                                                                                                                                                                                                                                     US2002137081-A1.
                                                                                                                                                                                                                                              Homo sapiens,
                                        26-FEB-2003
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ABX63473;
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Note: The sequence data for this patent did not form part of the specification, but was obtained in electronic format directly from USPTO at http.seqdata.uspto.gov/sequence.html?DocID=20020137081.
amount or distribution of the protein. The present sequence represents a cDNA of the invention that is differentially expressed in
                                                                                                                                                           Sequence 860 BP; 216 A; 211 C; 192 G; 241 T; 0 other;
                                                                                                                                                                                                                                 860
46
14
33
                                                                                                                                                                                                                                                      Matches:
Conservative:
Mismatches:
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227.00
64.52%
49.46%
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Percent Similarity: Best Local Similarity:

Score:

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256 AGGGCATGGTCTGCTCTTGCAGATTAGTATTCTGCCGGCGAACAGAACTTCGTGTTGGG 315
                                                         MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAlaGlu 20
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                                                                                                                                                                                                     61 LysglyLeulleÇyşHisÇysArgValLeuTyrCysılePheGlyGluHisLeuGlyGly 80
                                                                                                        41 AspValVallieTyrPheSerGlyAspAspSerCysSerLeuGlnValProGlySerThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A probe (D5' oligo) having the sequence given in AAQ53219 (claimed) was used to screen a population of clones to identify novel defensin defensin peptides. Pref. the libraries were human genomic and cDNA libraries. Hybridisation and partial sequence analysis of the identified clones contained previously characterised myeloid derived
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence encoding gastrointestinal defensin (GID) peptide called human defensin 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gastrointestinal defensin peptide(s) - useful as antimicrobial and anti-inflammatory agents and for detecting gastrointestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gastrointestinal defensin peptide; GID; pharmaceutical; Paneth cell; antimicrobial; anti-inflammatory; diagnosis; contact disinfectant; ss.
                                                                                                                                                                                                                                                                           316 AACTGCCTCATTGGTGGTGTGAGTTTCACATACTGCTGC 354
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                                 US-10-045-180A-3 (1-94) x ABX63473 (1-860)
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79 CCACTCCAAGCTGAGGATGATCCACTGCAGGCAAAAGCTTATGAGGCTGATGCCCAGGAG 138
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                                                                                                                                                                                                                                                                                                                                                                                                           MetArgThrleuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAlaGlu
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defensin sequences as well as new defensin related sequences. Two clones expressing new defensin related sequences were extensively characterised and found to contain genes selectively expressed in Paneth cells of the small intestin. These paneth cell-derived defensins are designated human defensin by and human defensins of the deaduced AA sequences of the defensin peptides. Comparison of the deduced AA sequences of the defensin 5 cDNA with the previously reported preprodefensisn shows significant similarity. The deduced AA sequence of defensin 6 cDNA has features similar to (Updated on 25-MAR-2003 to correct PN field.)
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114
29
29
                                                                                                                                                                                                       Sequence 452 BP; 123 A; 118 C; 98 G; 113 T; 0 other;
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Matches:
Conservative:
Mismatches:
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signalling pathway population; cancer; adenocarcinoma; leukaemia; immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray. Human signalling pathway polynucleotide probe SEQ ID NO 1198 Human; probe; ss; array element; Parkinson's disease; (INCY-) INCYTE GENOMICS INC 98US-0016434 98US-0016434 Homo sapiens 30-JAN-1998; 30-JAN-1998; US6500938-B1 31-DEC-2002 

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The invention relates to a combination which, comprises a number of polynucleotide probes comprising a sequence selected from one of the 1490 sequences mentioned in the specification. The combination is useful as an array element in a microarray for monitoring the expression of a number of target polynucleotides. The microarray is particularly useful in the diagnostics and immunopathology and neuropathology. The microarray is useful in diagnostics and immunopathology and neuropathology. The microarray is also useful for forensics and pharmacogenomics. The microarray is also useful for monitoring progression of diseases and for developing sophisticated profiles for the effects of currently available therapeutic drugs. The combination is also useful for purifying a subpopulation of mRNRs, conds and genomic fragments and in research and diagnostic applications. The array can detect changes in expression in a large number of genes coding controls signaling pathway populations which can be used to diagnose various diseases including cancer e.g. adenocarcinoma and leukaemia.

Conditional sidnaling pathway neuropathies e.g. Alzheimer's disease cod my Parkinson's disease. The present sequence represents a polynucleotide monter the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probe of the invention.

Note: The sequence data for this patent did not form part of the printer specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=06500938B1.
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                            useful as array
ion of a number o
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                          probes, use
expression
                                                                                                                       Claim 1; SEQ ID NO 1198; 65pp; English
                    Combination of polynucleotide microarray for monitoring the
                                                                         polymucleotides
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452 449 14 29 8 Length:
Matches:
Conservative:
Mismatches: 96e-18 220.00 63.00% 49.00% Similarity: Percent Similarity: Best Local Similari Query Match: Alignment Scores: Pred. No.: Score:

US-10-045-180A-3 (1-94) x ACA56600 (1-452)

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198
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                                                                                                                     LeuGlnValProGlySerThrLysGlyLeuIleCysHisCysArgValLeuTyrCysIle 73
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                                         21 ---------ProleuGinAlaArgAlaHisGluMetProAlaGlnLys 33
             PheGlyGluHisLeuGlyGlyThrCysPhelleLeuGlyGluArgTyrProlleCysCys
MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAlaGlu
                                                                              GlnProProAlaAspAspGlnAspValValIleTyrPheSerGlyAspAspSerCysSer
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AAC04468 standard; cDNA; 478 BP RESULT 7

(first entry) 06-OCT-2000

AAC04468;

Human secreted protein 5' EST, SEQ ID NO: 8543.

Seilhamer JJ;

Au-Young J,

WPI; 2003-352189/33,

Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;

BP.

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AAQ14908 standard; cDNA; 498
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                                                                                                                                                                                                                                                                                                                                                                        The present sequence is one of a large number of 5' ESTB derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTB were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dry primed cDNA libraries. Such ESTB are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTB are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTB are also used in diagnostic, forensic, gene therapy and chromsone mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 CCACTCCAGGCAAGAGCTGATGAGGTTGCTGCAGCCCCGGAGCAGATTGCAGCGGGACATC 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProLeuGlnAlaArgAlaHisGluMet --- ProAlaGlnLysGlnProProAlaAspAsp 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59
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                                                                                                                                                                                                                                                                                                               diagnostic, forensic, gene therapy and chromosome mapping procedures
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to 5'ESTs and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     391 GGAACCTGCATCTACCAGGGAAGACTCTGGGCATTCTGCTGC 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlyThrCysPhelleLeuGlyGluArgTyrProlleCysCys 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 478 BP; 117 A; 129 C; 127 G; 101 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               478
1447
132
11
                                                                                                                                                                                                                                                                               nucleic acid that is a 5' expressed sequence alning cDNAs and genomic DNAs that correspond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
                                                                                                                                                                                                                    Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID 8543; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
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                                                                                                                                                                                                                    Duclert A,
gene therapy; chromosome mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.47e-17
218.50
64.89$
50.00$
                                                                                                                         21-FEB-2000; 2000EP-0200610.
                                                                                                                                                        99US-0122487
                                                                                                                                                                                                                   Dumas Milne Edwards J,
                                                                                                                                                                                                                                                   WPI; 2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                     (GEST ) GENSET
                                                                                                                                                        26-FEB-1999;
                              Homo sapiens
                                                            EP1033401-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                          06-SEP-2000
                                                                                                                                                                                                                                                                                                  obtaining
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DB:
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AAQ14908
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21 ProLeuGlnAlaArgAlaHisGluMet---ProAlaGlnLysGlnProProAlaAspAsp 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene probe for chronic myelogenous leukaemia - esp. useful for distinguishing myeloblastic crisis from lymphoblastic crisis
                                                                                   CML; Philadelphia chromosome; myeloid-related sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP; 118 A; 134 C; 122 G; 111 T; 13 other;
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132
132
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Matches:
Conservative:
Mismatches:
Indels:
                                            Chronic myelogenous leukaemia-derived mrs cDNA,
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                                                                                                                                                                                                                                                                          comments"
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                                                                                                                                                                                                     Location/Qualifiers
16..378
/*tag= a
/note= "see comments"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88US-0279451.
84US-0655942.
87US-0094099.
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218.50
64.89%
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42.51%
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/*tag= b
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TEXA ) UNIV OF TEXAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saunders GF, Mars WM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1991-361533/49.
                                                                                                               88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAR15222
                                                                                                               chromosome 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 498
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214 CCAGAAGTGGTTGTTTCCCTTGCATGGACGAAGCTTGGCTCCAAAGCATCCAGGCTCA 273
                                                                            274 AGGAAAAACATGGCCTGCTATTGCAGAGATACCAGCGTGCATTGCAGGAGAAACGTCGCTAT 333
      59
                                                          ThrLysGlyLeuileCysHisCysArgValLeuTyrCysilePheGlyGluHisLeuGly 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a method for examining allergic diseases. The method comprises: (a) determining the expression level of defensin 1 gene in the biological sample from a patient; and (b) comparing the expression level with that in the sample of a healthy individual. The method is for examining allergic diseases particularly atopic dermatitis and its diagnosis, which is also applicable in screening candidate compounds for remedies. The present sequence is the
                                                                                                                                                                                                                                                                                                                             Antiallergic, allergic disease; allergy; defensin 1; atopic dermatitis; human; gene; ds.
40 GlnAspValVallleTyrPheSerGlyAspAspSerCysSerLeuGlnValProGlySer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Examining allergic diseases by changes in expression levels of defensinl gene in peripheral blood monocytes as indication, also applicable in screening compounds for treating of allergic diseases
                                                                                                                                                334 GGAACCTGCATCTACCAGGGAAGACTCTGGGCATTCTGCTGC 375
                                                                                                                   GlyThrCysPhelleLeuGlyGluArgTyrProlleCysCys 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saito H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Human defensin 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kagaya S, Gunji S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 45-46; 57pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coding sequence for human defensin 1.
                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
94..378
                                                                                                                                                                                                                                                                                               Human defensin 1 coding sequence.
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JAPAN GEN AGENCY NATION
                                                                                                                                                                                                              BP
                                                                                                                                                                                                         ABQ80601 standard; DNA; 498
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/product=
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P-PSDB; ABB98494.
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                                                                                                                                                                                                                                                                    11-NOV-2002
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Conservative: Mismatches: Indels: Gaps:

1.55e-17 218.50 64.89% 50.00% 42.51%

> Percent Similarity: Best Local Similarity:

Query Match:

Alignment Scores:

Length: Matches:

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274 AGGAAAAACATGGCCTGCTATTGCAGAAAACCAGCGTCGCTAT 333
                                                                                                                                     .54 CCACTCCAGGCAAGAGCTGATGAGGTTGCTGCAGCCCCGGAGCAGATTGCAGCGGACATC 213
                                                                                                                                                                                              214 CCAGAAGTGGTTGTTTCCCTTGCATGGAAGGATGGAAGCTTGGCTCCAAAGCTTCGTGGTCTA
                                          20
                                                                                                        21 ProleuGlnAlaArgAlaHisGluMet --- ProAlaGlnLysGlnProProAlaAspAsp 39
                                                                                                                                                                                   29
                                                                                                                                                                                                                                                60 ThriyysGlyLeulleCysHisCysArgValLeuTyrCysIlePheGlyGluHisLeuGly 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, antianaemic, vulnerary, antiinflammatory, immunomodulator,
antiinfertility, cerebroprotective, cytostatic; rheumatic, gene therapy,
neuroprotective, antiparkinsonian; protein therapy, EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESTS). They can be used to stimulate cell growth, to regulate haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. Parkinson's disease. The present sequence is a coding sequence of the
                                  1 MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAlaGlu
                                                        94 ATGAGGACCCTCGCCATCCTTGCTGCCATTCTCCTGGTGGCCCTGCAGGCCCAGGCTGAG
                                                                                                                                                                          40 GlnAspvalVallleTyrPheSerGlyAspAspSerCysSerLeuGlnValProGlySer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  An isolated polynucleotide for treating diseases associated with its encoded polypeptide such as cancer and multiple sclerosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ren F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhao QA,
                                                                                                                                                                                                                                                                                                                                                        334 GGAACCTGCATCTACCAGGGAAGACTCTGGGCATTCTGCTGC 375
                                                                                                                                                                                                                                                                                                                    80 GlyThrCysPhelleLeuGlyGluArgTyrProlleCysCys 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhang J,
RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human coding sequence SEQ ID NO: 133.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Asundi V,
I, Drmanac
US-10-045-180A-3 (1-94) x ABQ80601 (1-498)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressed sequence tag; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                ВР
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Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                            ABN59722 standard; cDNA; 514
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Yang Y,
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Xue AJ,
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or coagulation disorders
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; genome mapping; gene therapy; food supplement; virus; fungus; cell-proliferative disorder; neurodegenerative disease; bacterial; Parkinson's disease; alsheimer's disease; autoimmune disease; multiple sclerosis; diabetes; genetic disorder; wound; burn; infection; arthritis; cytostatic; immunomodulator; nootropic; neuroprotective; antiparkinsonian; antidiabetic; immunosuppressive; dermatological; haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
                                                                                                                                                                                                    156
                                                                                                                                                                                                                                                 277 AGGAAAAACATGGCCTGCTATTGCAGAATACCAGCGTGCATTGCAGGAGAACGTCGCTAT 336
                                                                                                                                                                                                                                                                                                                  217 CCAGAAGTGGTTGTTTCCCTTGCATGGGACGAAAGCTTGGCTCCAAAGCATCCAGGCTCA
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                                                                                                                                                                                                                               ProLeuGlnAlaArgAlaHisGluMet---ProAlaGlnLysGlnProProAlaAspAsp 39
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                                                                                                                                                                      MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAlaGlu
                                                                                                                                                                                        ThriysGlyLeulleCysHisCysArgValLeuTyrCysIlePheGlyGluHisLeuGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                         Zhang J, Z
k, Wang Z,
                                                                                                                                                                                                                                                                                                                                                                                                       93
  other;
                                            GlyThrCysPhelleLeuGlyGluArgTyrProlleCysCys
                                                                     Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oodrich RW, Asundi V, Zha
Y, Yamazaki V, Chen R,
Wang D, Drmanac RT;
Seguence 514 BP; 138 A; 142 C; 118 G; 116 T; 0
                                         Length:
Matches:
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                                                                                                                                          US-10-045-180A-3 (1-94) x ABN59722 (1-514)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human polynucleotide SEQ ID NO 84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABZ11202 standard; cDNA; 652
                                        1.62e-17
218.50
64.89%
50.00%
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                                                                                    Similarity:
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                                                                    Percent Similarity:
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                          Alignment Scores:
Pred. No.:
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                                      No.:
                                                                                    Best Local
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TYPE THE STANDARD STA

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Human; genome mapping; gene therapy; food supplement; virus; fungus; cell-proliferative disorder; neurodegenerative disease; bacterial; Parkinson's disease; Alzheimer's disease; autoimmune disease; multiple solerosis; diabetes; genetic disorder; wound; burn; infection; arthritis; cytostatic; immunomodulator; nootropic; neuroprotective; antiparkinsonian; antidiabetic; immunosuppressive; dermatological; haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide; antiarthritic; gene; ss.
                                              The invention relates to an isolated polynucleotide (I) comprising a nucleotide sequence selected from any of 948 sequences (ABZ1119-ABZ12066) or their mature protein coding portion, active domain coding protein or complementary sequences. The polynucleotides are useful for identifying expressed genes or for physical mapping of human genome. The encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight markers, as a food supplement, for generating antibodies, in medical imaging, screening and diagnostic assays and for treating cell-proliferative disorders (cancer), neurodegenerative diseases (Parkinson's or Alzheimer's disease), autoimmune diseases (multiple sclerosis, dibebetes, lupue) genetic disorders, wound, burns, incision, disorders, platelet or coagulation disorders, wound, burns, incision,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    448
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                                                                                                                                                                                                                                                                                                                                                                                                                   paramitic), arthritis, etc. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAlaGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    389 CCAGAAGTGGTTGCTTGCATGGACGAAAGCTTGGCTCCAAAGCATCCAGGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ThriysGlyLeuIleCysHisCysArgValLeuTyrCysIlePheGlyGluHisLeuGly
                                                                                                                                                                                                                                                                                                                                                                                               ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal
Claim 1; SEQ ID NO 84; 1012pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAACCTGCATCTACCAGGGAAGACTCTGGGCCATTCTGCTGC 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 652 BP; 146 A; 185 C; 177 G; 144 T; 0 other;
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
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64.89%
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us-10-045-180a-3.rng

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Ren F;
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                                                                                                                                                                                                                                                                                                                                               Zhao QA, 1
Ghosh M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 65; 1012pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                               Zhang J, Zl
, Wang Z,
                                                                                                                                                                                                                                                                                                                                      Tang YT, Zhou P, Goodrich RW, Asundi V, Zha
Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R,
Wehrman T, Wang J, Wang D, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   platelet or coagulation disorders
                                                                                                                                                                   05-MAR-2002, 2002WO-US05095.
                                                                                                                                                                                                                           05-MAR-2001; 2001US-0799451
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002-759812/82
                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; ABP68966
                                                  WO200270539-A2.
Homo sapiens.
                                                                                                          12-SEP-2002
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The invention relates to an isolated polymucleotide (I) comprising a nucleotide sequence selected from any of 948 sequences
(ABZ11119-ABZ12066) or their mature protein coding portion, active domain coding protein or complementary sequences. The polymucleotides are useful for identifying expressed genes or for physical mapping of human genome. The encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight markers, as a food supplement, for generating antibodies, in medical imaging, screening and diagnostic assays and for treating cell-proliferative disorders (cancer), neurodegenerative diseases (Parkinson's or Alzheimer's disease), autoimmune diseases (multiple sclerosis, diabetes, lupus) genetic disorders, myeloid or lymphoid disorders, platelet or coagulation disorders, wound, burns, incision, ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal, parasitic), arthritis, etc.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO

Sequence 664 BP; 174 A; 168 C; 161 G; 161 T; 0 other;

ftp.wipo.int/pub/published\_pct\_sequences.

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MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAlaGlu 20
                                                                                                                                       21 ProLeuGlnAlaArgAlaHisGluMet---ProAlaGlnLysGlnProProAlaAspAsp 39
                                                                                                                                                                                                                     60 ThriyaglyLeulleCysHisCysArgValLeuTyrCysIlePheGlyGluHisLeuGly 79
                                                                                                                                                                                                                                                            80 GlyThrCysPhelleLeuGlyGluArgTyrProlleCysCys 93
           664
14
13
13
1
          Length:
Matches:
Conservative:
Mismatches:
                                                 Indels:
                                                                             US-10-045-180A-3 (1-94) x ABZ11183 (1-664)
          2.26e-17
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                                       Best Local Similarity:
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Alignment Scores:
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The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I') can have respiratory, bronchodilator, antinfinamatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodys receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adheason molecules and their receptors, cytokine and chemokine receptors, and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasociated proteins. The receptors, binding proteins and malignancy associated proteins. The receptors, binding proteins and malignancy associated proteins. The receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactort hypoproduction which are associated with a disease or condition and error including temperators.
                                                                                                                                                                                                                                                                                                          Now adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; respiratory obstruction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pain; cystic fibrosis; allergic rhinitis; chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating
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491 GGAACCTGCATCTACCAGGGAAGACTCTGGGGATTCTGCTGC 532
                                                                                                                                                                                                                                                                  Human defensin 3 polynucleotide fragment #2478.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancers and respiratory obstructions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 218; 1592pp; English.
                                                                                                                     AAF20911 standard; DNA; 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-MAR-2000; 2000WO-US08020
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                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer; 88.
                                                                                                                                                                    AAF20911;
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                                                                     RESULT 13
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150 ccacriccadecaadaadcigargagargagergergecadecegageageageageageageageare 209
                                                                                                                                                                                                                                                                                                                                                                             210 CCAGAAGTGGTTGCTTTCCCTTGCATGGGAAGGTTGGCTCCAAAGCTTCCAGAGCTTA 269
                                                                                                                                                                                                                                                                                                                                                                                                                                     40 GlnAspValValIleTyrPheSerGlyAspAspSerCysSerLeuGlnValProGlySer 59
                                                                                                                                                                                                                                         MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAlaGlu 20
                                                                                                                                                                                                                                                                                                  21 ProleuglinAlaArgAlaHisGluMet --- ProAlaGlnLysGlnProProAlaAspAsp 39
                                                                                                                                                                                                                                                                                                                                                                                                                    60 ThrLysGlyLeulleCysHisCysArgValLeuTyrCysilePheGlyGluHisLeuGly 79
and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; adenosine receptor; low adenosine antisense oligonuclectide; phosphorothicate; impaired respiration; inflammation; allergy; allergy; disease; bronchoconstriction; inhibitor; antiinflammatory; antiallergic antiasthmatic; cytosetatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain, cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human adenosine receptor related polynucleotide SEQ ID NO:2478.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          330 GGAACCTGCATCTACCAGGGAAGACTCTGGGCATTCTGCTGC 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93
                                                            Sequence 464 BP; 110 A; 128 C; 119 G; 107 T; 0 other;
                                                                                                       464
744
132
132
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                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                    2.49e-17
216.50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                the present invention.
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                                                                                                                Score:
Percent Similarity:
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                                                                                      Alignment Scores:
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e.g. ischaemic conditions, pulmonary vasoconstriction, allergies asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONs reduces side effects. The A-containing ONs break down with the release of deoxyadenosine which activates adenosine receptors causing bronchocomstriction and inflammation. AAA32313 to AAA35312 represent the nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 185, but the sequences of differ from the previously named sequences. SEQ ID NO:11 to 1680 (AAA33232 to AAA33392) are specifically claimed ONs from the present invention. N.B. Sequences given in the disclosure of the present invention door match up with their corresponding SEQ ID NO: sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90 Ardakdakcicircecarciriecreciarricirciraridareciradaseciradada 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a new composition comprising an antiesnse oligonuclectide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammacory, antiallergic, antialtengic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 ProLeuGlnAlaArgAlaHisGluMet---ProAlaGlnLysGlnProProAlaAspAsp 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAlaGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210 CCAGAAGTGGTTGTTTCCCTTGCATGGGAGAGAAGCTTGGCTCCAAAGCATCCAGGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 ThriyaGlyLeulleCysHisCysArgValLeuTyrCysilePheGlyGluHisLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 GlnAspValValIleTyrPheSerGlyAspAspSerCysSerLeuGlnValProGlySer
  bronchitis, emphysema, respiratory distress syndrome, ischemia or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         330 GGAACCTGCATCTACCAGGGAAGACTCTGGGCATTCTGCTGC 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 464 BP; 110 A; 128 C; 119 G; 107 T; 0 other;
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147
132
114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                        Disclosure; Page 612; 1343pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     given in the sequence listing.
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26-OCT-2000. 

human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory, bronchodilator; antinflammatory; immunosuppressive; antiasthmatic; analgasic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cytlic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis; Low adenosine antisense oligonucleotide; phosphorothioate; allergy; cancer; 88.

Homo sapiens.

WO200062736-A2.

24-MAR-2000; 2000WO-US08020.

99US-0127958. 06-APR-1999;

(UYEC-) UNIV EAST CAROLINA.

(NYCE/) NYCE J W.

Nyce JW;

WPI; 2000-679539/66.

Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions -

Disclosure; Page 217-218; 1592pp; English.

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiliflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with carporating the factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and activity and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific anymes, binding proteins, adenosine molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vascociated proteins. The anticluding respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactoral phyporoduction which are sescitated with a disease or condition and peripheral wascondered with a disease or condition and peripheral response associated proteins. condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention.

Sequence 644 BP; 110 A; 182 C; 184 G; 140 T; 28 other;

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1147
                Matches:
Conservative:
Mismatches:
         Length:
                                        Indels:
                                               Gaps:
       3.83e-17
216.50
64.89%
50.00%
42.12%
                              Best Local Similarity:
                       Percent Similarity:
Alignment Scores:
Pred. No.:
Score:
                                      Query Match:
DB:
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OM protein

Run on:

Sequence:

Searched:

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Sequence 14, Appl
Sequence 13, Appl
Sequence 1047, Ap
Sequence 18198, A
                                                                                                                                                                                                                                                                                                                    Sequence 16, Appl
Sequence 12, Appl
Sequence 122, App
Sequence 124, App
Sequence 120, App
Sequence 120, App
Sequence 141529,
Sequence 7, Appli
Sequence 7, Appli
Sequence 28, Appli
                                                                           473, App
223, App
16, App
78, App
78, App
11, App
13, App
13, App
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Sequence 141528,
Sequence 141530,
Sequence 141528,
Sequence 141528,
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Sequence 48280, 7
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Sequence 48284,
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Sequence 2, Application US/10013770
Publication No. US20020113151A1
GENERAL INFORMATION:
APPLICANT: GENSET SA
TITLE OF INVENTION: HUMAN DEFENSIN DEF-X GENE AND DNAC
COMPOSITION CONTAINING SAME AND DIAGNOSTIC AND THERAPEUTIC APPLICATIONS
                                                   Sequence 1
                                                                                            Sequence Sequence Sequence Sequence Sequence
                                   equence
                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
US-10-013-770-2
US-10-045-180A-2
US-10-045-180A-1
US-10-045-180A-1
US-10-045-180A-1
US-10-045-180A-1
US-10-045-180A-1
US-10-044-090-473
US-09-186-828-16
US-10-141-645-14
US-10-141-645-14
US-10-141-645-14
US-09-18-995-18198
US-09-18-995-18198
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US-10-027-632-141530
US-10-027-632-30053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
   CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe,
STREET: 550 West C
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STATE: California
COUNTRY: USA
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-Q=/Cgn2 1/USPTO spool p/US10045180/runat 17122003 145026 12635/app_query.fasta_1.860
-Q=/Cgn2 1/USPTO spool p/US10045180/runat 17122003 145026 12635/app_query.fasta_1.860
-DB=Published Applications_NA -OFMT=fastap -SUPETX=rnpb -MINATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bite -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSTZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10045180 @GGN 1 1.74 @runat 17122003 145026 12635
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG $GCRES=0 -MATT -DSPBLOCE=100
-LONGLOG -DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                            2003, 15:06:18; Search time 325 Seconds (without alignments) 963.776 Million cell updates/sec
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| Cgn2_6/ptodata/2/pubpna/US07 PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/PCT_NBW PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/PCT_NBW PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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| Cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
       GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                 - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                   hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Maximum DB seq length: 200000000
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Match Length DB
                                                                                              December 17,
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                   APPLICANT: Bougueleret, Lydie
APPLICANT: Chumakov, 11ya
APPLICANT: Chumakov, 11ya
TITLE OF INVENTION: Human Defensin Polypeptide Def-X, Genomic DNA and cDNA, Compositi
TITLE OF INVENTION: Containing Them and Applications to Diagnosis and to Therapeutid
TITLE OF INVENTION: Containing Them and Applications to Diagnosis and to Therapeutid
TITLE OF INVENTION: UNUMBER: US/10/045,180A
CURRENT APPLICATION NUMBER: US 09/486,580
PRIOR APPLICATION NUMBER: US 09/486,580
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: PC7/FR98/01864
PRIOR FILING DATE: 1998-08-28
PRIOR FILING DATE: 1998-08-28
PRIOR FILING DATE: 1998-08-29
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
TENNOTURE AFE
                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/10045180A Publication No. US20020182703A1 GENERAL INFORMATION:
TYPE: DNA
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REGISTRATION NUMBER: 40,637
REFERENCE/DOCKET NUMBER: GEN
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 453 BASE PAIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: LINEAR MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 09/486,580
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 10-Dec-2001 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCTGCTTCATCCTTGGTGAACGCTACCCAATCTGCTGCTAC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ThrCysPheIleLeuGlyGluArgTyrProIleCysCysTyr 94
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/10013770

Publication No. US20020115151A1

GENERAL INFORMATION:
APPLICANT: GENSET SA

APPLICANT: GENSET SA

COMPOSITION CONTAINING SAME AND DIAC

THERAPEUTIC APPLICATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
FEATURE:
PEATURE:
NAME/KEY: CDS
LOCATION: (52)..(336)
OTHER INFORMATION: Def-X coding sequence
             REFERENCE/DOCKET NUMBER: GENSET.064C1
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4415 BASE PAIRS
                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/013,770
FILING DATE: 10-Dec-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Knobbe, Martens, Olson & Bear
STREET: 550 West C Street
CITY: San Diego
STATE: California
                                                                                                                       APPLICATION NUMBER: 09/486,580 FILING DATE: <Unknown>
ATTORNBY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                     ZIP: 92101
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172 GATGTGGTCATTTACTTTTCAGGAGATGACAGCTGCTCTCTTCAGGTTCCAGGCTCAACA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 CCGCTCCAGGCAAGAGCTCATGAGATGCCAGCCCAGAAGCAGCCTCCAGCAGATGACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        292 ACCTGCTTCATCCTTGGTGAACGCTACCCAATCTGCTGCTAC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    232 AAGGGCTTGATCTGCCATTGCAGAGTACTATACTGCATTTTTTGGAGAACATCTTGGTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 LysGlyLeuIleCysHisCysArgValLeuTyrCysIlePheGlyGluHisLeuGlyGly 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAlaGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AspValValIleTyrPheSerGlyAspAspSerCysSerLeuGlnValProGlySerThr 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProLeuGlnAlaArgAlaHisGluMetProAlaGlnLysGlnProProAlaAspAspGln 40
                                                                                                         NAME: Hart, Daniel
TYPE: NUCLEOTIDE
                                                                                     REGISTRATION NUMBER: 40,637
                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
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Matches:
Conservative:
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Indels:
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; NAME/KEY: polyadenylation site; LOCATION: 4374..4379; SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-10-013-770-1
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DB:
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Best Local Similarity:
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                                3406 ATGAGGACCCTCACCCTCTCTGCCTTTCTCCTGGTGGCCCTTCAGGCCTGGGCAGAG
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MOLECULE TYPE: DNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                       3586 TGCCAGCATGCAGAGCTACAGACTAGACAGAAGGACAGGACAGGCTCTGGAATTGGAT 3645
                                                                                                                                                         3766 ATTCCAAGATATGACTGTGAAATTCACTAGATTTAAGATATAAGGAGATGCTACCTAGTT 3825
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                                                                                             CCTTCTGGAGCCAGACAAACAAGCTTAAGTATATAGGAAAATATTTCACCCTGTCTATAT 3885
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4161..4380
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3394..3577
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4276..4278
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1836..1874
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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US-10-045-180A-1
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SEQ ID NO 1
LENGTH: 4415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bougueleret, Lydie
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Human Defensin Polypeptide Def-X, Genomic DNA and cDNA, Composit1
TITLE OF INVENTION: Containing Them and Applications to Diagnosis and to Therapeutic
TITLE OF INVENTION: Containing Them and Applications to Diagnosis and to Therapeutic
TITLE OF INVENTION: Containing Them and Applications to Diagnosis and to Therapeutic
TITLE OF INVENTION: CONTAINING THE US/10/045,180A
CURRENT ETLING DATE: 2001-10-18
PRIOR APPLICATION NUMBER: US 09/486,580
PRIOR APPLICATION NUMBER: POT/FR98/01864
PRIOR APPLICATION NUMBER: POT/FR98/01864
PRIOR FILING DATE: 1998-08-28
PRIOR FILING DATE: 1998-08-28
PRIOR FILING DATE: 1997-08-29
PRIOR FILING DATE: 1997-08-29
PRIOR FILING DATE: 1997-08-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/10045180A Publication No. US20020182703A1 GENERAL INFORMATION:
                                   FEATURE:

NAME/KEY: misc feature

TOTATION: (1111)...(1111)
                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (670)..(670)
OTHER INFORMATION: n =
                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(4415)
                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (143)..(143)
OTHER INFORMATION: n =
                                                                                                                                                                                                                                                                          LOCATION: (85)...(85)
OTHER INFORMATION: n =
                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature LOCATION: (85)...(85)
NAME/KEY: misc_feature
                                                                                          OTHER INFORMATION: n =
                                                                                                           NAME/KEY: misc_feature
LOCATION: (970)..(970)
                                                                                                                                                                                                                                                                                                                                   LOCATION: (1). (4415)
OTHER INFORMATION: Def-X
                    FEATURE:
                                OTHER INFORMATION: n =
                                                                                                                                                                                                                                                                FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4126 CCCGTACTCAGTTTCTGATGCTCTCTCTGGGTCCCCAGGCTCAACAAAGGGCTTGATCTG 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4006 CTCTGTGTATTTATTCCTATTGACTGAGATTGTTTGTGCTACCGGCTGTAATACAGCCAA 4065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3946 AGGAATGCAGAAAAGTGAAGCAAAGGAGAATGAGTCTCGAATCCTGTGTGACCAGCACTG 4005
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FEATURE:
NAME/KEY: misc feature
LOCATION: (3406)...(3408)
OTHER INFORMATION: Translation
                                                                                                                                                 NAME/KEY: misc feature LOCATION: (3394)..(3577) OTHER INFORMATION: Exon
                                                                                                                                                                                                        NAME/KEY: misc feature LOCATION: (3391)...(3393) OTHER INFORMATION: splic
                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (2710)..(2780)
OTHER INFORMATION: L1 fragment
                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (2367)..(2367)
OTHER INFORMATION: n = a,
                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (2191)...(2191)
OTHER INFORMATION: n = a,
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                          OTHER INFORMATION: splice FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (2155)..(2335)
OTHER INFORMATION: Alu insertion
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (1875)..(1880)
OTHER INFORMATION: splice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: TATA signal LOCATION: (1758)..(1767) OTHER INFORMATION:
                                                     NAME/KEY: misc feature LOCATION: (3578)..(358
                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (2186)..(2186)
OTHER INFORMATION: n = a,
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OTHER INFORMATION: n = a,
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LOCATION: (2117)...(2117)
OTHER INFORMATION: n = a,
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LOCATION: (1974)..(1974)
OTHER INFORMATION: n = a,
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LOCATION: (1711)..(1714)
OTHER INFORMATION:
 LOCATION:
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OTHER INFORMATION: n = a
          NAME/KEY: misc_feature
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LOCATION: (2133)..(2133)
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Best Local Similarity:
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LOCATION: (4274)...(4276)
OTHER INFORMATION: Translation
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LOCATION: (4161)...(4163)
OTHER INFORMATION: splice
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LOCATION: (4374)..(4379)
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4006 CTCTGTGTATTTATTCCTATTGACTGAGATTGTTTGTGCTACCGGCTGTAATACAGCCAA 4065
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                                                                                                                                                                                                                                                                            CTCAGTGGCAGATGTCACTTAGGTGGCTATACTTAACATCTCTGGTCCTGGATTTTCTCA 3705
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                                                     AGGAATGCAGAAAAGTGAAGCAAAGGAGAATGAGTCTCGAATCCTGTGTGACCAGCACTG 4005
                                                                                                                                                                CCTTCTGGAGCCAGACAAACAAGCTTAAGTATATAGGAAAATATTTCACCCTGTCTATAT 3885
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US-10-045-180A-3 (1-94) x US-10-045-180A-8 (1-542)
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CURRENT FILING DATE: 2001-10-18
PRIOR APPLICATION NUMBER: US 09/486,580
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: PCT/FR98/01864
PRIOR FILING DATE: 1998-08-28
PRIOR FILING DATE: 1997-08-29
PRIOR FILING DATE: 1997-08-29
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TITLE OF INVENTION: Human Defensin Polypeptide Def-X,
TITLE OF INVENTION: Containing Them and Applications
FILE REFERENCE: GEN-100D1
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SOFTWARE: PatentIn version 3.1
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ORGANISM: Homo
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LOCATION: (52)..(345)
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                                                                                                                  GACATATCTATTTCCTTTGCATGGATAAAAGCTCTGCTCTTCAGGTTTCAGGCTCAACA
  ThrCysPheIleLeuGlyGluArgTyrProIleCysCys 93
                                                                                                                                                                                              CCACTCCAGGCAAGAGGTGATGAGGCTCCAGGCCAGGAGCAGCGTGGGCCAGAAGACCAG
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                                                                                     | Sequence 223, Application US/10252157
| Publication No. US20030190640A1
| GENERAL INFORMATION:
| APPLICANT: Faris, Mary
| APPLICANT: Pearson, Cecelia I.
| TITLE OF INVENTION: GENES EXERESSED IN PROSTATE CANCER
| FILE REFERENCE: PA-0027-1 US
| CURRENT APPLICATION NUMBER: US/10/252,157
| CURRENT APPLICATION NUMBER: 60/295,048
| PRIOR APPLICATION UMBER: 60/295,048
| PRIOR PILING DATE: 2001-05-31
| NUMBER OF SEQ ID NOS: 501
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; OTHER INFORMATION: Inc:
US-10-044-090-473
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SEQ ID NO 223
LENGTH: 555
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TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTMARE: PERL PROGram
SEQ ID NO 473
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ORGANISM: Homo sapiens
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Alignment Scores
                                  US-09-816-828-16
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                                                                                                                            NUMBER OF SEQ ID NOS: 18
SOFTWARE: pt FL genes Version 2.0
SEQ ID NO 16
LENGTH: 726
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APPLICANT:
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TITLE OF INVENTION: No. US20020150898A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 791CIP2E
CURRENT APPLICATION NUMBER: US/09/816,828
CURRENT FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR APPLICATION NUMBER: 09/752,929
PRIOR APPLICATION NUMBER: 09/552,929
PRIOR APPLICATION NUMBER: 09/552,929
PRIOR APPLICATION NUMBER: 09/552,929
PRIOR FILING DATE: 2000-04-18
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                                                NAME/KEY: CDS
LOCATION: (151)..(522)
                                                                                 FEATURE:
                                                                                           ORGANISM: Homo
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030190640A1 903338.12
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Zhang, Jie
Wang, Jian-Rui
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Zhou, Ping
Zrich, Ryle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ThrLysGlyLeuIleCysHisCysArgValLeuTyrCysIlePheGlyGluHisLeuGly 79
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APPLICANT: Wehrman, Tom
APPLICANT: Wehrman, Tom
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
TITLE OF INVENTION: No. US2003002329A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 791C1P2ADIV
CURRENT APPLICATION UNMBER: US/10/125,237
CURRENT FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 09/68,317
PRIOR APPLICATION NUMBER: 09/68,317
PRIOR FILING DATE: 2000-09-2
PRIOR APPLICATION NUMBER: 09/52,929
PRIOR APPLICATION NUMBER: 09/52,929
PRIOR APPLICATION NUMBER: 09/552,929
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 91
SOPTWARE: pt_FL_genes Version 2.0
SEQ ID NO 78
                                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1143)
US-10-125-237-78
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Best Local Similarity:
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US-10-125-237-78
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Publication No.
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Liu, Chenghua
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Xue, Aidong J.
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Ren, Feiyan
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o. US20030022329A1
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Percent Similarity:
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US-10-105-891-78
; Sequence 78, Application US/10105891
; Publication No. US20030073099A1
                                                                                                                       US-10-045-180A-3 (1-94) x US-10-105-891-78 (1-1348)
                                                                                                                                                                                                                                                                              Alignment Scores:
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US-10-105-891-78
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CURRENT APPLICATION NUMBER: US/10/105,891

CURRENT FILING DATE: 2002-03-25

PRIOR APPLICATION NUMBER: 09/668,317

PRIOR FILING DATE: 2000-09-22

PRIOR APPLICATION NUMBER: 09/552,929

PRIOR FILING DATE: 2000-04-18

NUMBER OF SEQ ID NOS: 91
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TITLE OF INVENTION: No. US20030073099Alel Nucleic Acids
TITLE OF INVENTION: Polypeptides
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APPLICANT: Liu, Chenghua
APPLICANT: Zhou, Ping
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
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     21 ProLeuGlnAlaArgAlaHisGluMet---ProAlaGlnLysGlnProProAlaAspAsp
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                                                                 1 MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAlaGlu
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Wehrman, Tom
Wang, Jian-Rui
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Xue, Aidong J.
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Ren, Feiyan
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Best Local Similarity:
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SEQ ID NO 1
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APPLICANT: Alan Wa
APPLICANT: Alexand
APPLICANT: Teresa
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Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 496
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (124)...(304)
OTHER INFORMATION: retro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 60/284,855
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: Unassigned
PRIOR FILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
FILE REFERENCE: UCLA-001CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1039 AGGAĀĀAACATGGACTĠĊTATŤĠĊĀĠĀATACCAGCGTĠĊĀŤŤGCĀĠĠĀĠĀĀCGTCGCTAT 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1099 GGAACCTGCATCTACCAGGGAAGACTCTGGGCATTCTGCTGC 1140
                                                         256 GCGAGAGGCTTGAGGTGCATTTGCGGAAGAGGAATTTGCCGGTTTGTTATAACGTCGCTTT 315
                                                                                                                                                                                                             136 GAGCCACTTCAGGCAAGAGCTGATGAAGCTGCAGCCCAGGAGCAGCCTGGAGCAGATGAT
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80 GlyThxCysPheIleLeuGlyGluArgTyrProIleCysCys 93
                                                                                           60 ThrLysGlyLeuIleCysHisCysArgValLeuTyrCysIlePheGlyGluHisLeuGly 79
                                                                                                                                                                     40 GlnAspValVallleTyrPheSerGlyAspAspSerCysSerLeuGlnValProGlySer 59
                                                                                                                                                                                                                                     20 GluProLeuGlnAlaArgAlaHisGluMetProAlaGlnLysGlnProProAlaAspAsp 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FastSEQ for Windows Version
                                                                                                                                 CAGGAAATGGCTCATGCCTTTACATGGCATGAAAGTGCCGCTCTTCCGCTTTCAGACTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alexander Cole
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o. US20030144184A1
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34.14%
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RESULT 13
US-10-313-994-13
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DB:
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Best Local Similarity:
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TITLE OF INVENTION: Retrocyclins - Antiviral
TITLE OF INVENTION: Antimicrobial Peptides
FILE REFERENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 60/284,855
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: Unassigned
PRIOR APPLICATION NUMBER: Unassigned
PRIOR APPLICATION NUMBER: Unassigned
PRIOR FILING DATE: 2001-04-18
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APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alexander Cole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14, Application US/10141645
Publication No. US20030144184A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version SEQ ID NO 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: mat_peptide
IOCATION: (287)...(313)
OTHER INFORMATION: ligated to RTD1b in head-to-tail orientation to
OTHER INFORMATION: form the cyclic octadecapeptide RTD1; RTD1 is
OTHER INFORMATION: stabilized by three intramolecular disulfides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: sig_peptide
LOCATION: (95)...(154)
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OTHER INFORMATION: theta defensin lA precursor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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                                                            329
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165.50
56.57%
45.45%
32.20%
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICANT: Tang, Yi-Quan

APPLICANT: Yuan, Jun

APPLICANT: Ouellette, Andre J.

TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of I

FILE REFERENCE: P-UC 3095

CURRENT APPLICATION NUMBER: US/10/313,994

CURRENT FILING DATE: 2002-12-05

PRIOR APPLICATION NUMBER: US/09/309,487

PRIOR FILING DATE: 1999-05-10

NUMBER OF SEQ ID NOS: 31

SOPTWARE: Patentin Ver. 2.0

SEQ ID NO 13

LENGTH: 500
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; Sequence 1047, Application

; Patent No. US-20020168637A1

; GENERAL INFORMATION:
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                                                                  APPLICANT:
                                                                                                     APPLICANT:
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APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
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FEATURE:
NAME/KEY: CDS
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                                                                                                 Carter, Darrick
Retter, Marc
Mannion, Jane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ThrLysGlyLeuIleCys-------HisCysArgValLeuTyrCysIlePhe 74
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                                                                                                                                                     Vedvick, Tom
                                                                                                                                                                                          Bangur, Chaitanya
Lodes, Michael A.
                                                                                   Fan, Liqun
                                                                                                                                                                        Fanger, Gary
                                                                                                                                                                                                                               Wang, Tongtong
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56.57%
45.45%
32.20%
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APPLICANT: Marnerakis, Margarita
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Vedvick, Thomas S.
APPLICANT: Wedvick, Thomas S.
APPLICANT: McNabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILLE REFERENCE: 210121.478CT;
CURRENT APPLICATION NUMBER: US/09/902,941
CURRENT FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 2002
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1047
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US-09-902-941-1047/c
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Best Local Similarity:
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NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1047
LENGTH: 412
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
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                                           TYPE: DNA
ORGANISM: Homo sapiens
FEATURE: NAME/KEY: misc_feature LOCATION: 183, 271, 28
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LOCATION: (1)...(412)
OTHER INFORMATION: n = A,T,C
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ORGANISM: Homo sapien
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Watanabe, Yoshihiro
Johnson, Jeffrey C.
Retter, Marc W.
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Matches:
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Search completed: December 17, 2003, 21:35:57
Job time: 330 secs

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Result
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Maximum DB
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Listing first 45 summaries
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-DB=ISSUed_Patents_NA -QFMT=fastap_-SUFFIZ=rni -MINNATCH=0.1 -LOOPCIE-0
-LOOPEXT=0 -UNITS=bite STRAT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DCCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10045180 @CGN 1 1 193 @runat 17122003 145024 12553 -NCPU=6 -TCPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XOAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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-MODEL=frame+_p2n.model -DEV=xlp
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441.383 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                           /cgn2 6/ptodata/2/ina/5A_COMB.seq:*
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US-08-158-189-6

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US-08-486-013-46

US-08-482-279-46

US-08-482-279-46

US-08-915-968-46

US-09-015-968-46

US-09-015-968-46

US-08-486-013-54

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Sequence 2, Appli
Sequence 1, Appli
Sequence 6, Appli
Sequence 1198, Ap
Sequence 46, Appli
Sequence 46, Appli
Sequence 46, Appl
Sequence 54, Appl
Sequence 54, Appl
Sequence 54, Appl
                                                                                                                                                                                    Description
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US-09-486-580A-2
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245678800112245378788001122
       MOLECULE TYPE:
                    TOPOLOGY: LIN
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## ALIGNMENTS

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US-09-486-580A-2
US-09-486-580A
Sequence 2, Application US/09486580A
Sequence 2, Application US/09486580A
Sequence 2, Application US/09486580A
Sequence 2, Application:
APPLICANT: GENSET SA
APPLICANT: GENSET SA
APPLICANT: GENSET SA
APPLICANT: GENSET SA
ITILE OF INVENTION: HUMAN DEFENSIN DEF-X GENE AND DNAC
ITILE OF INVENTION: THERAPEUTIC APPLICATIONS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 550 West C Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/486,580A
FILLING DATE: FEBRUARY 25, 2000
ATTORNEY/AGENT INFORMATION:
NAME: Hart, Daniel
REGISTRATION NUMBER: GENSET.064C1
REGISTRATION NUMBER: GENSET.064C1
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 453 BASE PAIRS
TYPE: NUCLECTIDE
STRANDEDNESS: DOUBLE
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
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RESULT 2
US-09-486-580A-1
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Query Match:
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                                                                                                         APPLICATION NUMBER: US/09/486,580A
FILING DATE: FEBRUARY 25, 2000
ATTORNBY/AGENT INFORMATION:
NAME: Hart, Daniel
REGISTRATION NUMBER: 40,637
REFERENCE/DOCKET NUMBER: GENSET.064C:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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APPLICANT: GENSET
                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                        MOLECULE TYPE:
ORIGINAL SOURCE:
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ADDRESSEE: Knobbe, Marteni
STREET: 550 West C Street
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FEATURE:
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          ORGANISM: Homo sapiens
                                                                STRANDEDNESS:
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                                                                                             4415 BASE PAIRS
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Query Match:
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US-09-486-580A-1
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                                                                                                                     ATTCCAAGATATGACTGTGAAATTCACTAGATTTAAGATATAAGGAGATGCTACCTAGTT 3825
                                                                                                                                                                                                                                                                                        TGCCAGCATGCAGAGCTACAGACTAGACAGAAGGACAGGAGACAGGCTCTGGAATTGGAT 3645
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                                                                                                                                                                           CCTTCTGGAGCCAGACAAACAAGCTTAAGTATATAGGAAAATATTTCACCCTGTCTATAT 3885
                                                             AGGAATGCAGAAAAGTGAAGCAAAGGAGAATGAGTCTCGAATCCTGTGTGACCAGCACTG 4005
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3406..3408
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3394..3577
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1836..1874
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4276..4278
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RESULT 3
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US-10-045-180A-3 (1-94) x US-08-158-189-6 (1-452)
                                Query Match:
DB:
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GENERAL INFORMATION:
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                                                                                                                                                                FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PM PC PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bevins, Charles L.
APPLICANT: Jones, Douglas E.
TITLE OF INVENTION: Gastrointestinal Defensin Peptides,
TITLE OF INVENTION: CDNA Sequences, Methods for Production and Use Thereof
                                                                                                                                                                                                                                                                                                                   TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                            NAME: Johnson, Philip S.
REGISTRATION NUMBER: 27,200
REFERENCE/DOCKET NUMBER: CH-0219
                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                   LENGTH: 452 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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RESULT 4
US-09-016-434-1198
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Best Local Similarity:
                                                           Pred. No.:
                                                                           Alignment Scores:
                                                                                                                  US-09-016-434-1198
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Patent No. 6500938
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APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-O
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: PRIOR APPLICATION NUMBER:
                                                                                                                                                   IMMEDIATE SOURCE:
LIBRARY: GENBANK
                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
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                                                                                                                                   CLONE:
                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: sing
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CITY: PALO ALTO
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                                                                                                                                                                                                                                           452 base pairs
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                                                                                                                                                                                                                                                                                                                                                            PA-0002 US
                   Length:
Matches:
Conservative:
 Mismatches:
149
29
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US-08-158-189-4
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DB:
Alignment Scores
                                      US-08-158-189-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                         FEATURE:
                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5641497ris
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bevins, Charles L
APPLICANT: Jones, Douglas E.
                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                    NAME/KEY:
LOCATION:
                                                                                                    TOPOLOGY:
                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                               NAME: Johnson, Philip S.
REGISTRATION NUMBER: 27,200
REFERENCE/DOCKET NUMBER: CH-0219
                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
                                                                                                                                          TYPE:
                                                                                                                                                                                                              TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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o. 5641497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 PheGlyGluHisLeuGlyGlyThrCysPheIleLeuGlyGluArgTyrProIleCysCys 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34
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Best Local Similarity:
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Patent No. 57
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                                                                   TELEFAX: (619) 535-89
INFORMATION FOR SEQ ID NO:
                                                                                                             REFERENCE/DOCKET NUMBER: 31,815
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CITY: San Diego
CTATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 14-AUG-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: UPILING DATE: 18-NOV-1
APPLICATION NUMBER: UPILING DATE: UPILING DATE:
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APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
TITLE OF INVENTION: of Their Use
                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                         FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACCTTGCTATCTCCTTTGCAGGAAATGGACTCTCTGCTCTTAGAACCTCAGGTTCTCAG 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCACTCCAGGAAAGAGCTGATGAGGCTACAACCCAGAAGCAGTCTGGGGAAGACAACCAG 129
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420 base pairs
                                                                                                         (619) 535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Campbell and Flores
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47.31%
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RESULT 7
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
        FILING DATE:

FILING DATE:

CLASSIFICATION: 530
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/342,268
FILING DATE: 18-NOV-1994
APPLICATION NUMBER: US 07/930,649
FILING DATE: 14-AUG-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/889,020
FILING DATE: 26-MAX-1992
ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL
                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC comp
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Selsted, Michael E.
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antibiotic Cryptdin Peptides
TITLE OF INVENTION: of Their Use
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,27
                                                                                                                                                                                                                                                                                                                                                      CITY: San Diego
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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EDNESS: double
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4370 La Jolla Village Drive, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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Indels:
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 46,
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US-08-342-268-46
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Best Local Similarity:
Query Match:
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TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                    STREET: 43.
STREET: 43.
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Selsted, Michael E.
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
TITLE OF INVENTION: of Their Use
                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 14-AUG-1992
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CORRESPONDENCE ADDRESS:
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                                                                                                                        APPLICATION NUMBER: US/08/342,268 FILING DATE: 18-NOV-1994 CLASSIFICATION: 435
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4370 La Jolla Village Drive,
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                 US 07/889,020
                                                                              07/930,649
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DB:
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AMME: Campbell, Cathryn A.
REGIGTRATION NUMBER: 31, 815
REFERENCE/DOCKET NUMBER: P-UC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 46:
                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6057425
                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Ovellette, Andre J.
TITLE OF INVENTION: Antibiotic Cryptdin Peptides and
TITLE OF INVENTION: of Their Use
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                 CITY: San Diego
STATE: California
                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221
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173.50
55.91%
40.86%
33.75%
   US 08/482,279
                                                                      US/09/015,968
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Indels:
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US-09-397-386-46; Sequence 46, A
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Best Local Similarity:
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                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                              GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
PILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                     APPLICANT: Selsted, Michael E.
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
TITLE OF INVENTION: of Their Use
NUMBER OF SEQUENCES: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: P-UC 3003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPROX: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 18-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
COMPUTER READABLE FORM
                                                                                                                    CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER:
                  COUNTRY: 7212
                                                STREET: 4370 La Jolla Village
CITY: San Diego
STATE: California
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                                                                                                     ADDRESSEE:
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                                                                                   Drive,
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; Sequence 54, Application; Patent No. 5731149; GENERAL INFORMATION: APPLICANT: Selsted;
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Best Local Similarity:
Query Match:
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FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 9-UC 3003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/342,268
FILLING DATE: 18-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,649
FILING DATE: 14-AUG-1992
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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TOPOLOGY: li
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FILING DATE: 07-JUN-1995
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OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER: I
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                                 54, Application US/08486013
o. 5731149
                                                                                                                                 81 ThrCysPheIleLeuGlyGluArgTyrProIleCysCys 93
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   Selsted, Michael E.
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Percent Similarity:
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Pred. No.:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve;
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,013
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US 08/342,268
FILING DATE: 18-NOV-1994
APPLICATION NUMBER: US 07/930,649
FILING DATE: 14-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,020
FILING DATE: 14-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,020
FILING DATE: 26-MAY-1992
ATTORNET/AGENT INFORMATION:
NAME: Camphell Cathern
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TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 54:
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LENGTH: 401 base pairs
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell
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TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
TITLE OF INVENTION: of Their Use
NUMBER OF SEQUENCES: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UC
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    263
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California
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  ACCTGCAGAAAGGGTCATTTATTGTACACTCTCTGCTGT
                                 ThrCysPheIleLeuGlyGluArgTyrProIleCysCys
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4370 La Jolla Village Drive, Suite 700
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US-08-482-279-54
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Patent No. 5840498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: p-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
TITLE OF INVENTION: of Their Use
NUMBER OF SEQUENCES: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 26-MAY-1992 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 18-NOV-1
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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California
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                              Percent Similarity:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/88s
FILING DATE: 26-MAY-1992
ATTORNEY, AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Selsted, Michael E.
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
TITLE OF INVENTION: of Their Use
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APPLICATION NUMBER: US 07/930,649
FILING DATE: 14-AUG-1992
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: California
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US-10-045-180A-3 (1-94) x US-09-015-968-54 (1-401)
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 0
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 07-7UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 18-NOV-1994
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                               NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UC 3003
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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70 La Jolla Village Drive, Suite
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14-AUG-1992
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                                            3.43e-13
171.50
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Matches:
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US-09-397-386-54
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Patent No. 6300470
GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
TITLE OF INVENTION: of Their Use
                                            TELEFAX: (619) 535-894:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/482,279
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/342,268
FILING DATE: 18-NOV-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,81
                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 14-AUG-PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                               REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
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CITY: San Diego
TYPE: nucleic acid
STRANDEDNESS: doub
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                                            81 ThrCysPheIleLeuGlyGluArgTyrProIleCysCys 93
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Command line parameters:

-MODEL-frame+ p2n.model -DEV=xlp
-Q-/cgn2 1/USPTO_spool_p/US10045180/runat_17122003_145023_12528/app_query.fasta_1.860
-Q=/cgn2 1/USPTO_spool_p/US10045180/runat_17122003_145023_12528/app_query.fasta_1.860
-DB=GenEmbl -QFMT-fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCI=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MN0= -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US10045180_@CGN 1_1 5283 @runat_17122003 145023 12528 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEDUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
-DEV_TIMEDUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5
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41: em htgo-mus:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

### Result No. იიი იი 333310Score Query Match Length 100.0 4415 128544 1232180 232180 452 3060 79730 150940 158653 168702 169044 195 479 479 5302 5320 5321 110 1110 1110 1110 203 203 203 멂 HUMDFSNSIX HSU33317 AF314060 RABMCP1AA RABMCP1AA RABMCP1AB AR021138 I49589 RABNPCS4A RABMCP1A BD174049 HUMDEF1AA AX405718 BC027917 AF188268 AF188269 AF188270 BD074745 AF238378 ä HUMDEFB HSDEF3 BD028213 174645 179691 149591 149592 149590 AX405993 S55582 AF205406 AF200455 AR270635 AC021883 A98571 AF184160 I49596 AC079018 **I49588** HUMDEF1A AF184159 I33694 HSHP1 ACO79018 Homo sapi AF205406 Homo sapi 149590 Sequence 8 119589 Sequence 8 110841 Oryctolagus M28883 Rabbit macr M28884 Rabbit macr AF28072 Rabbit macr AF28073 Rabbit macr AF2973 Rabbit macr AF2973 Requence 9 174645 Sequence 9 174645 Sequence 9 174645 Sequence 10 149591 Sequence 10 149591 Sequence 10 149592 Sequence 10 149593 Sequence 38 AF188269 Macaca mu AF188269 Macaca mu AF188270 Macaca mu AF188150 Macaca mu AF184150 Macaca mu M98331 U33317 AF314060 Homo sapi AF233439 Homo sapi AF200455 Homo sapi AX405993 Sequence AR270635 Sequence AF238378 Homo A98570 Sequence 1 BD074745 Human def A98571 Sequence Description I49588 AC021883 Homo sapi AX405718 Sequence BC027917 Homo sap BD174049 Method of M26602 Human defen Homo sapien Human defen Sequence 6 Sequence 2 Human def sapi

ALIGNMENTS

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                           GENSET

OS Homo sapiens (human)

PN JP 2001514264-A/2

PD 11-SEP-2001

PF 28-AUG-1998 JP 2000508701

PF 29-AUG-1997 FR 71/10823

PI LYDIS BOUGUSLERET, ILYA SHMACOV

PC C07K14/435,A01N43/50,A01N63/00,A61K7

PC A61P37/02,C07K16/18,C12N1/15,C12N1/1

PC A61P37/02,C07K16/18,G1N33/53,A61K37/

PC C12P21/02,

PC C12P21/08,C12Q1/68,G01N33/53,A61K37/

Strandedness: Double;
CC Topology: Linear;
CC Topology: Linear;
CC Human defensin polypeptide Def-X, ge
composition

CC Contribution
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BOUGUELERET, L. and Chumakov, I.

HUMAN DEFENSIN DEF-X, GENE AND DNAC, COMPOSITION CONTAINING AND DIAGNOSTIC AND THERAPEUTIC APPLICATIONS

Patent: WO 9911663-A 2 11-MAR-1999;

BOUGUELERET LYDIE (FR); CHUMAKOV ILYA (FR)

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                      Human defensin polypeptide Def-X, genome DNA and cDNA, composition containing the same, and application to diagnosis and remedy Patent: JP 2001514264-A 2 11-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 453)
Bougueleret, L. and Shmacov, I.
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containing the same, and application to diagnosis and remedy
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pr 2001514264-A/2
11-SEP-2001
28-AUG-1998 JP 2000508701
29-AUG-1997 FR 97/10823
LYDIE BOUGUELERET, ILYA SHMACOV
COTKIA/435,A01N43/50,A01N63/00,A61K7/00,A61K38/00,A61P29/00,
                                                                                                          C12P21/08, C12Q1/68, G01N33/53, A61K37/02, C12N15/00
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Sequence 1 from Patent WO9911663.
A98570.1 GI:6781626
         BD074745

4415 bp DNA linear PAT 27-A Human defensin polypeptide Def-X, genome DNA and cDNA, compocontaining the same, and application to diagnosis and remedy
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                                                                                                                                                                                                                                                                                                                                                                                               Bougueleret,L. and Chumakov,I.
HUMAN DEFENSIN DEF-X, GENE AND DNAG, COMPOSI
AND DIAGNOSTIC AND THERAPEUTIC APPLICATIONS
PALENT: WO 991163-A 1 11-MAR-1999;
BOUGUELERET LYDIE (FR); CHUMAKOV ILYA (FR)
LOCATION/Qualifiers
treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unidentified
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                                                                                                   MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAla 19
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
/db_x1874
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AF238378/c
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OS Homo sapiens (hume pn JP 2001514264-A/1 pd 11-SEP-2001 pr 2001514264-A/1 pd 11-SEP-2001 pr 28-AUG-1997 pr 29-AUG-1997 pr 17714/435,A01143, pc A61935/00, pc A61937/02,COTK16/1 C12P21/02, C12P21/08, C12P1/08, C12P1/08
                                                                                                                                                                                                                                                     sequence.
AF238378
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 128544)
Polley, A., Baumgart, C., Blechschmidt, K., Dette, M.D.,
Menzel, U., Reichwald, K., Schilhabel, M.B., Schudy, A.,
                                                                                                                                                                                                                                                                                                          AF238378 128544 bp
Homo sapiens chromosome 8 clone
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Human defensin polypeptide Def-X, genome DNA and cDNA, composition containing the same, and application to diagnosis and remedy Patent: JP 2001514264-A 1 11-SEP-2001;
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BD074745.1 GI:226
JP 2001514264-A/1.
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                                                                                                                                          Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                   sapiens (human)
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C07K14/435, A01N43/50, A01N63/00, A61K7/00, A61K38/00, A61P29/00,
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29-AUG-1997 FR 97/10823
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p22-p21, complete
                                                                                                             Euteleostomi;
        Taudien, S.,
                                                                                       Homo.
                               Jahn, N.,
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                  This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (02-APR-2003) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany
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6 (bases 1 to 128544)
Lagemann, D. and Platzer, M.
Direct Submission
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Lagemann, D. and Platzer, M.
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Direct Submission
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Direct Submission
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Unpublished
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Rosenthal, A.
assembly was confirmed by restriction digest.
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                                                                                                                                                                                                                            Sequencing vector: pUC18; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of re Assembly program: Phrap; version 0.990329 Consensus quality: 127999 bases at least Q40 Consensus quality: 128330 bases at least Q30 Consensus quality: 128544 bases at least Q20
                                                                                                                                                                                                            Quality coverage: 11.05x
                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: H370
Center clone name: SCb-561b17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: gscj-submit@genome.imb-jena.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Insitute of Molecular Biotechnology Center code: IMB
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COMMENT

Sequence Quality Assessment: Quality levels above 40 are 1 error in 10,000 bp. This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to qual Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN.1 file. /organism="Homo sapiens" /mol\_type="genomic DNA" /db\_xref="taxon:9606" /chromosome="8" Location/Qualifiers 128544 expected to have to quality zero

FEATURES

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AC021883.4 GI:9910096
HTG; HTGS PHASE1
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 232180)
Waterston, R.H.
                                                                                   Homo sapiens (human)
          The sequence of Homo sapiens clone 
Unpublished
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Direct Submission

Submitted (21-JAN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality coverage: 6.35 in Q20 bases; agarose-fp Quality coverage: 4.69 in Q20 bases; sum-of-contigs
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On Aug 25, 2000 this sequence version replaced gi:9838290.
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                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 40 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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          Tang, Y.T., Liu, C., Zhou, P., Asundi, V., Zhang, J., Xue, A.J., Yang, Y., Wehrman, T. and Drmanac, R.T. Novel nucleic acids and polypeptides Patent: WO 0222660-A 408 21-MAR-2002; HYSEQ, INC. (US)
                                                                                                                        Homo sapiens (human)
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Sequence 408 from Patent
AX405993
                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Au-Young, J. and Seilhamer, J.J.
Composition for the detection of signaling pathway gene expression
Patent: US 6500938-A 1198 31-DEC-2002;
Location/Qualifiers
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Bevins, C.L. and Jon
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/db_xref="GI:21439426"
/translation="MRTLTILTAVLLVALQAKAEPLQAEDDPLQAKAYEADAQEQRGA
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/mol_type="genomic DNA"
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1 (bases 1 to 452)

Jones, D.E. and Bevins, C.L.

Defensin-6 mRNA in human Paneth cells: implications for antimicrobial peptides in host defense of the human bowel FEBS, Lett. 315 (2), 187-192 (1993)
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	/um Aler   caxous 2000   /um Aler   caxous 200	/Organism='Homo sapiens" /mol type="genomic DNA" /db Tref."t=yon.0606"		of this entry's ASN.1 file.	Base-by-base grows we have are not generally visible from the GenBank flat file format but are available as narr	Qualify duries wasts have been reduced to qualify zero.  Qualification above 40 are expected to have less than  1 error in 10 000 hm		Sequence Quality Assessment: This entry has been annotated with sequence quality	assembly was confirmed by restriction digest.	as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one pUC18 subclone: and the	chemistry, or covered by high quality data (i.e., phred quality >=	This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate		Consensus quality: 79729 bases at least Q20	at least	ig Dye;	Sequencing vector: pHC18: 100% of reads	Center project name: H376 Center clone name: Ou-L-i2046	Contact: gscj-submit@genome.imb-jena.de	Web site: http://genome.imb-jena.de/	Center: Insitute of Molecular Biotechnology	COMMENT On Jul 9, 2002 this sequence version replaced gi:10998844.	Biotechno	Direct Submission  Submitted (09-IIII-2002) Genome Analysis Institute of	REFERENCE 3 (bases 1 to 79730)  AUTHORS Lagemann.D. and Platzer.M.	JOURNAL Submitted (17-OCT-2000) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany			TITLE Chromosome 8 genomic sequence	Wen,G., Schutte,B., Malik,M., Peng,J.Hong., McCray,P. and Rosenthal.A.	AUTHORS Polley, A., Baumgart, C., Blechschmidt, K., Dette, M.D., Jahn, N., Menzel, U., Reichwald, K., Schilhabel, M.B., Schudy, A., Taudien, S.,	rammaria; Eurreria; Frimaces; Cacarrinni; Hominidae; 1 (bases 1 to 79730)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E	S S	ACCESSION AF314060 VERSION AF314060.2 GI:21717333 KEYMORDS HTG	sequence.	_
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                                                                                                                                                                                                                                                                                                                                                       Submitted (01-APR-2003) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany On Apr 1, 2003 this sequence version replaced gi:29336172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (28-MAR-2003) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany (bases 1 to 150940)
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Lagemann, D. and Platzer, M.
Direct Submission
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Lagemann, D. and Platzer, M.
Direct Submission
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Direct Submission

Submitted (24-MAY-2000) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany

(bases 1 to 150940)

Reichwald, K. and Platzer, M.

Direct Submission
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Schudy, A., Schilhabel, M., Baumgart, C.,
Schattevoy, R. and Rosenthal, A.
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AF233439 AF166112
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Center project name: H350
Center clone name: CTD-2629116
Center clone name: CTD-2629116
Center clone name: CTD-2629116
Center clone name: CTD-2629116
Sequencing vector: pUC18; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 150881 bases at least Q40
Consensus quality: 150926 bases at least Q30
Consensus quality: 150940 bases at least Q20
Quality coverage: 22.17x
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                                                                                                                                                                                                                                    Center: Insitute of Molecular Biotechnology Center code: IMB Center code: IMB Web site: http://genome.imb-jena.de/Contact: gscj-submit@genome.imb-jena.de
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a 07745, Germany
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

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Sequence Quality Assessment:
This entry has been annotated with sequence quality computed by the Phrap assembly program

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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                    sequence.
AF200455
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Homo sapiens chromosome 8 clone
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Schudy,A., Schilhabel,M., Schutte,B., Malik,M., Hong Peng,J., McCray,P., Baumgart,C., Menzel,U., Weber,J., Schattevoy,R. an Rosenthal,A.
                                                                                             Maumalia; Butheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 158653)

Schudy, A., Blechschmidt, K., Menzel, U., Polley, A., Reichwald, K., Rump, A., Schilhabel, M.B., Taudien, S., Wen, G., Schutte, B., Malik, M. Peng, J. Hong., McTay, P. and Rosenthal, A.

Peng, J. Hong., McTay, P. and Rosenthal, A.

Chromosome B genomic sequence
                                                                                                                                                                                                                                           Homo sapiens
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38626. .38692
/note="single stranded/single chemistry region
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33223 c 36391 g 41958 t
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93393. .93395
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Mismatches:
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Direct Submission
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Biotechnology, Beutenbergstr. 11, Jena 07745,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
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Center clone name: SCb-540n10
Center clone name: Statistics
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14120. .14203
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|550. .1558
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TITLE
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KEYWORDS
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                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                 Homo sapiens chromosome
AC079018
   Iliev,I., Johnson,R., Jones,C.,
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We 8, clone RP11-161B1, complete sequence.
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Mismatches:
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FEATURES	TITLE JOURNAL COMMENT	TITLE JOURNAL REFERENCE AUTHORS	TITLE JOURNAL REFERENCE AUTHORS
Web site: http://www-seq.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu	Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  Direct Submission Submitted (15-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 15, 2002 this sequence version replaced gi:22123231. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (196-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html	Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  Direct Submission  [AL Submitted (06-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  [CE 4 (bases 1 to 168702)  4 (bases 1 to 168702)  Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Farreira, J., Charg, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Ferreira, P., FittGerald, M., Gage, D., Galagan, J., Gardham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meddrim, J., Meneus, I., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Ngayen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Schupback, R., Seaman, S., Severy, P., Schuth, S., Schupback, R., Seaman, S., Schupback, R., Seaman, S., Schupback, R., Seaman, S., Schupback, R., Seaman, S., Schupback, R., S	Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Menous, L., Mihova, T., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Olivar, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Rieback, M., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Mu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.  Direct Submission  L. Submitted (15-AUG-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  Direct Submission  L. Submitted (15-AUG-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, N., Bastien, V., Bloom, T., Boguslavkly, L., Boukhgalter, B., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farro, S., Farreita, P., FitzGerald, M., Gage, D., Galagan, J., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Kartas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., WacLean, C., Macdonald, P., Major, J., Meneus, L., Mihova, T., Mlenga, V., MucLean, C., Macdonald, P., Major, J., Metthews C., Rogov, P., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Pierre, N., Parker, P., Pie
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78.95%
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0,
Fgapop 6.0,
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Copyright (c) 1993 - 2003 Compugen Ltd.
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### 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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# ALIGNMENTS

REFERENCE AUTHORS	ORGANISM	ACCESSION VERSION KEYWORDS	LOCUS DEFINITION	RESULT 1 BF895944/c
Mammalia; Eutheria; Frimaces; Catarrhin; Hominidae; Homo. 1 (bases 1 to 221) Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,	Homo sapiens (numan) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	BF895944.1 GI:12287403 BF895944.1 GI:12287403	BF895944 221 bp mRNA linear EST 18-JAN-2001 CM2-MT0157-221100-548-b02 MT0157 Homo sapiens cDNA, mRNA sequence.	

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SOURCE
ORGANISM
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DEFINITION
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Bukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 168)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOllveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                        168 bp mRNA linear CM0-MT0390-070201-767-b09 MT0390 Homo sapiens cDNA, E1023130
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                                                                                                                                                                                                                        Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: +55-11-2704922
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Ludwig Institute for Cancer Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAla 19
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/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
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Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington, Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith,B., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random activation of gene expression
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
                                                                                                                                                                                                                                                                                                                                                                           1 MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAla 19
                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
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BG193795.1
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This sequence was derived from the FAPESD/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CMO&t2=CMO-MT0390-
070201-767-b09&t3=2001-02-07&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 15
High quality sequence stop: 168.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: +55-11-2704922
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                                                                                                                                                                                                                                                                          Athersys RAGE Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
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                                                                                                                                                     Chordata;
Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                  l (bases 1 to 243)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagari,M.A., ta Silva,W. Jr. Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Fax: +55-11-2707001
Email: asimpsom@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3&t2=QV3-MT0129-
111100-419-c11&t3=2000-11-11&t4=1)
                                                                                                                                                                              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
                                                                                                                                                                                                 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                          Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                        Tel: +55-11-2704922
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                                                                                                                                                                                                                                                                                                                                            sequence tags
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Contact: Scott J.
Athersys, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 216 431 9900
Fax: 216 361 9596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: scain@athersys.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MetArgThrLeuThrLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAla 19
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Location/Qualifiers
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/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
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/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
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Matches:
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Indels:
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Query Match:
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                                                                                                                                                                                                       CE 1 (bases 1 to 251)

RS Adams, M.D., Kerlavage, A.R., Pleischmann, R.D., Fuldner, R.A., Bult (C.J., Lee, N.H., Kirkness, B.F., Weinstock, K.G., Gocayne, J.D., White, C.J., Lee, N.H., Kirkness, B.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man. Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, B., Hinkle, P.S. Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Werrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Fhillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dinke, D., Feng, D.F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.M., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon Venter, J. G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 ATGAGGACCCTCGCCATCCTTGCTGCCATTCTCCTGGTGGCCCTGCAGGCCCAGGCT 100
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Contact: Kerlavage, AR
                                                                                                       Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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EST23992 Bone marrow Homo sapiens cDNA 5'
                            Other_ESTs: THC169174
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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High quality sequence star
                                                                                                                                                                                           Venter, J.C.
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/clone lib="MT0129"
/note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

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/mol_type="mRNA"
/db_xref="taxon:9606"
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Best Local Similarity:
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                                                                                                                                                 E 1 (bases 1 to 281)

S Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult
, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White
, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A.,
Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald
, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A.,
Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weddman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, B.J.,
Dinke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W. M.,
Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L.,
Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L.,
Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon
Venter, J. C.
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                                                                  Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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Other_ESTs: THC169174
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGAGGACCCTCGCCATCCTTGCTGCCATTCTCCTGGTGGCCCTGCAGGCCCAGGCT
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/dev_stage="adult"
/clone_lib="Bone_marrow"
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/db_xref="ATCC (inhost):122061"
/db_xref="laxon:9606"
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Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
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/clone_lib="Bone marrow"
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Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
Information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                  1 (bases 1 to 290)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA
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                                                                                 Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                              Contact: Simpson A.J.G.
                                                                                                                                                                                                                    sequence tags
                                                                                                                                                                                                                                          Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                 Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
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                                                           Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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+55-11-2707001
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/dev_stage="adult"
/clone_lib="Bone marrow"
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|mol_type="mRNA"
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RESULT 9
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CB 1 (bases 1 to 294)

RS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult

C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White

,C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White

,C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White

,C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White

,C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Man-Wai, C., Clayton, R.A.,

Cline, T.R., Cotton, M.D., Earle-Hughes, J., Finc, L.D., Fitzgerald

,L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A.,

Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.M.,

Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Nguyen, D.T., Nguyen, D.T.,

Moreno-Palanques, R
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl7tl=QV3&t2=QV3-GN0107-
111100-423-a12&t3=2000-11-11&t4=1)
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Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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/mol type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="GN0107"
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RESULT 10
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1 (bases 1 to 298)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult (C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White (O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald (L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Shirley, R., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.M., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Weit, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, W.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and
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EST23847 Bone marrow Homo sapiens cDNA 5' end similar to defensin
based upon 83 million nucleotides of cDNA sequence
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For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi/html)

    mRNA sequence.

                     Initial assessment of human gene diversity and expression patterns
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Contact: Kerlavage, A
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/dev_stage="adult"
/clone_lib="Bone marrow"
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/mol_type="mRNA"
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/db_xref="taxon:9606"
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3 EST23896 Bone marrow Homo
1, mRNA sequence.
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Contact: Kerlavage, AR
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/dev_stage="adult"
/clone lib="bone marrow"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
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/mol_type="mRNA"
/db_xref="ATCC (inhost):121926"
/db_xref="taxon:9606"
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RESULT 12
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

22 1 (bases 1 to 320)

RS Adams, M.D., Karlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S. Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L.,
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Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
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Contact: Kerlavage, AR
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Medical Center Drive, Rockville,
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/db_xref="ATCC (inhost):121974"
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/dev_stage="adult"
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/sex="mixed"
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|mol_type="mRNA"
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/note="Vector: pBluescript SK-;
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RESULT 13
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Bukaryofa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 327)

28 Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man.Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
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9712 Medical Center Drive, Rockville, MD 20850 USA
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/dev_stage="adult"
/clone_lib="Bone marrow"
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/mol_type="mRNA"
/db_xref="ATCC (inhost):121998"
/db_xref="taxon:9606"
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                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bages 1 to 348)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., 2ago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
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QV3-MT0129-111100-427-h01 MT0129
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For clone availability, additional sequence and exinformation related to this EST, please check the Index (http://www.tigr.org/tdb/hgi/hgi.html)
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Contact: Kerlavage, AR
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/mol_type="mRNA"
/db_xref="ATCC (inhost):122063"
/db_xref="taxon:9606"
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/clone_lib="Bone marrow"
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                                                                                                                                                     1 (bases 1 to 349)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3&t2=QV3-MT0129-
111100-427-h01&t3=2000-11-11&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 348.
Location/Qualifiers
Contact: Simpson A.J. Laboratory of Cancer
                                                                                                                  Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CM3-MT0343-170101-665-a05
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                 sequence tags
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                                     10737800
                                                                          Proc. Natl. Acad.
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BASE COUNT
ORIGIN
Search completed: December 17, 2003, 18:25:43 Job time : 665.293 secs
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DB:
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                                                                                                                                                                                                                          1 MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAla 19
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.hudwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-MT0343-
170101-665-a05&t3=2001-01-17&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 349.
Location/Qualifiers
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Fax: +55-11-2707001
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0, Y
Fgapop 6.0, F
Delop 6.0, F
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                      BLOSUM62
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

# SUMMARIES

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LP321 [		DNA fragment SYN-U	n pre-pro	92-mer used in con	92mer used in cons		c-myc 1	GENSET codi	Human defensin 5 D	3			factor-rela		cDNA differ	defensin 1	adenosine r	defensin 3	polynucleot		defensin 3			₽	human codin	Human defensin 1 c	ic myeloge	secreted t	adenosine r		Himan gene signatii			pre-pro	110-mer used in co	110mer used in con		Sequence encoding		Human intestine sp	eotide seg	sequence	cDNA sequence enco	ription

### ALIGNMENTS

## RESULT 1 AAX26697

AAX26697 standard; cDNA; 453 ВР

AAX26697;

18-JUN-1999 (first entry)

cDNA sequence encoding human defensin (Def-X) protein.

AIDS; immune Human defensin; Def-X; antimicrobial; antiparasitic; pesticide; cytostatic; anticancer; inflammation; tissue repair; endocrine regulation; corticostatic regulation; deficiency; psoriasis; ss. cancer; melanoma;

Homo sapiens.

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RESULT 2
AAX26698
ID AAX26
XX
XX
AC AAX2
XX
XX
DT 18-U
DT CDNP
XX
XX
WW CDNP
XX
XX
Huma
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Huma
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                                                                                                                                                                                                                                                                                                                                                          US-10-045-180A-4 (1-19) x AAX26697 (1-453)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of inflammation, tissue repair and endocrine (especially conticostatic) cregulation. The polypeptide can be used in a composition for external topical use, especially in a cosmetic composition. Compositions containing Def-X can be used for prevention and treatment of microbial and parasitic infections, especially where the microbial or parasitic infections are Gram-positive or -negative bacterial infections or mycobacterial, fungal or spirochaete infections, or where the viral infections are associated with enveloped viruses, especially HSV and HIV. The compositions can used for prevention and/or treatment of cancers, especially melanomas, or liver cancer, prostate cancer, non-small-cell lung cancer or colorectal carcinoma, and for enhancing immunity, especially in the case of AIDS, or preventing immune deficiency, inflammatory processes, especially in the case of chronic inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a pesticide. The Def-X polypeptide can be used as a cytostatic (especially anticancer) agent, and as an agent for modulating processes of inflammation, tissue repair and endocrine (especially corticostatic)
                                                                            Human defensin; Def-X; antimicrobial; antiparasitic; pesticide; cytostatic; anticancer; inflammation; tissue repair;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence encodes human defensin (Def-X). The Def-X polypeptide can be used as an antimicrobial, antiparasitic agent or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 3; 56pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-AUG-1997;
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               Homo sapiens
                                             endocrine regulation; corticostatic regulation; cancer; melanoma;
AIDS; immune deficiency; psoriasis; ss.
                                                                                                                         cDNA sequence encoding human defensin (Def-X) protein
                                                                                                                                                             18-JUN-1999
                                                                                                                                                                                                                             AAX26698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FR2767832-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  defensin polypeptide Def-X - useful as antimicrobial agent,
ancer agent, pesticide, etc.
                                                                                                                                                                                                                                                                                             52
                                                                                                                                                                                                                                                                                                         1 MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAla 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY01604.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         453
                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP; 107
                                                                                                                                                             (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97FR-0010823
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90.00
100.00%
100.00%
20
                                                                                                                                                                                                                         CDNA; 453
                                                                                                                                                           entry)
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                        453
19
0
0
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The present sequence encodes human defensin (Def-X). The Def-X

controlled can be used as an antimicrobial, antiparasitic agent or

a pesticide. The Def-X polypeptide can be used as a cytostatic

(especially anticancer) agent, and as an agent for modulating processes

of inflammation, tissue repair and endocrine (especially corticostatic)

cregulation. The polypeptide can be used in a composition for external

containing Def-X can be used for prevention and treatment of microbial

and parasitic infections, especially where the microbial or parasitic

infections are Gram-positive or -negative bacterial infections or

mycobacterial, fungal or spirochaete infections, or where the viral

infections are associated with enveloped viruses, especially HSV and HIV.

The compositions can used for prevention and/or treatment of cancers,

cespecially melanomas, or liver cancer, prostate cancer, non-small-cell

lung cancer or colorectal carcinoma, and for enhancing immunity,

cespecially in the case of AIDS, or preventing immune deficiency,

cespecially in the treatment of psoriasis, as well as for modulating

inflammatory processes, especially in the case of Chronic inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anticancer agent,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human defensin polypeptide Def-X - useful as antimicrobial agent,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bougueleret L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Fig 4; 56pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chumakov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pesticide, etc.
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Sequence 453 BP; 107 A; 121 û 97 ဝှ 128 T; 0 other;

0	Mismatches:		Best Local Similarity:
0	Conservative:	100.00%	Percent Similarity:
19	Matches:	90.00	Score:
453	Length:	1.09e-06	Pred. No.:
			Alignment Scores:

US-10-045-180A-4 (1-19) x AAX26698 (1-453)

#### RESULT 3

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AAX26696 standard; DNA; 4415 BP

# AAX26696;

18-JUN-1999 (first entry)

Nucleotide sequence of human defensin (Def-X).

Human defensin; Def-X; antimicrobial; antiparasitic; pesticide; cytostatic; anticancer; inflammation; tissue repair; endocrine regulation; corticostatic regulation; cancer; melanom cancer; melanoma;

immune deficiency; psoriasis;

Homo sapiens.

FR2767832-A1

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ARBSULT 4
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ID AAHH
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XX AAHE
XX AAHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence encodes human defensin (Def-X). The Def-X CD polypeptide can be used as an antipharastic agent or CC a pesticide. The Def-X polypeptide can be used as a cytostatic cof inflammation, tissue repair and as an agent for modulating processes CC of inflammation, tissue repair and endorine (especially corticostatic) cregulation. The polypeptide can be used in a composition for external containing bef-X can be used for prevention and treatment of microbial containing Def-X can be used for prevention and treatment of microbial containing Def-X can be used for prevention and treatment of microbial containing Def-X can be used for prevention and treatment of microbial containing Def-X can be used for prevention and treatment of parasitic infections or parasitic infections or parasitic infections or parasitic infections are associated with enveloped viruses, especially HSV and HIV. The compositions can used for prevention and/or treatment of cancers, capacially melanomas, or liver cancer, prostate cancer, non-small-cell lung cancer or colorectal carcinoma, and for enhancing immunity, capacially in the case of AIDS, or preventing immune deficiency, capacially in the treatment of psoriasis, as well as for modulating inflammatory processes, especially in the case of chronic inflammatory
                                                                                                                                      lung; liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss; metabolic disease; developmental disease; cytostatic; immunomodulatory; neuroprotective; gene therapy; cancer; immunopathology; neuropathology.
                            WO200132927-A2
                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                   Human intestine specific cDNA sequence SEQ ID NO:60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH57220 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4415 BP; 1128 A; 1109
                                                                                                                                                                                                                                         Human; tissue specific; diagnosis; brain; heart;
                                                                                                                                                                                                                                                                                                                                                                         10-SEP-2001
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90.00
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          000019
                                                                                                                                                                                                                                         skeletal muscle;
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequences (I). (I) can have cytostatic, immunomodulatory and neuroprotective activities, and can be used in gene therapy. (I) and proteins (II) encoded by then are used in high throughput screening assays to select DNA molecules, RNA molecules, peptide nucleic acids, mimetics, peptides, proteins, agonists, antagonists, antibodies or their fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical agents Expression of (I) in a sample indicates the differentiation of embryonic stem cells into a tissue selected from brain, heart, kidney, liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used to produce an expression profile that defines a metabolic or developmental process, treatment, condition, disease or disorder. The gene profile can be used for diagnosis, predisposition to a disorder where the gene is associated with a
                                                                                                                       Human; antianaemic; vulnerary; antiinflammatory; immunomodulator; antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy; neuroprotective; antiparkinsonian; protein therapy; EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New cell and tissue specific polynucleotides useful for diagnosis, prognosis or monitoring of treatments for disorders where the gene associated with a cancer, immunopathology or neuropathology -
                                                                                                             expressed
                                                                                                                                                                                     Novel human
                                                                                                                                                                                                               28-JUN-2002
                                                                                                                                                                                                                                            ABN59997;
                                                                                                                                                                                                                                                                       ABN59997 standard; cDNA; 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 95; 327pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INCY-) INCYTE GENOMICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunopathology or neuropathology.
                                                                                                                                                                                                                                                                                                                                         MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAla
                                                                                                                                                                                                                                                                                                                             ATGAGAACCCTCACCATCCTCACTGCTGTTCTCCTCGTGGCCCTCCAGGCCAAQGCT
                                                                                                             sequence
                                                                                                                                                                                  coding sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP;
                                                                                                                                                                                                              (first entry)
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64.00
89.478
78.95%
71.11%
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                                                                                                                                                                                                                                                                       ΒP
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                                                                                                                                                                                                                                                                                                                                                                                       (1-294)
                                                                                                                                                                                  ID NO:
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Matches:
Conservative:
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Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 T; 5 other;
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10-SEP-2001; 2001WO-US26015

21-MAR-2002. WO200222660-A2 Homo sapiens

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RRESULT 6
AAQ53217
ID AAQ53217
AC AAQ5
AC AAQ5
AC AAQ5
AC AAQ5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESTs). They can be used to stimulate cell growth, to regulate haematopoisesis e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemastasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.
                                                                                                                                                                                                                                                                                                                                             Gastrointestinal defensin peptide; GID; cell; antimicrobial; anti-inflammatory; contact disinfectant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An isolated polynucleotide is encoded polypeptide such as
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                                                                                                                                                                                                                                                                                               Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence encoding gastrointestinal defensin (GID) peptide called human defensin 6\,\cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 398 BP; 102 A; 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2003
17-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ53217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ53217 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parkinson's disease. The present sequence is a coding sequence of the
     22-MAY-1992;
                                                18-MAY-1993;
                                                                                                                                                  WO9324513-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002-292408/33.
DB; ABB97584.
                                                                                                                                                                                                                                                                                               sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptide such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGAGAAACCCTCACCATCCTCACTGCTGTTCTCCTCGTGGCCCTCCAGGCCAAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAla 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (updated)
(first entry)
     92US-0888232
                                                   93WO-US04740.
                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                           /*tag=
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Wehrman
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64.00
89.47%
78.95%
71.11%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for treating diseases associated cancer and multiple sclerosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Asundi V,
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Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                       pharmaceutical;
diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              other;
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Gastrointestinal defensin peptide(s) - useful as antimicrobial and anti-inflammatory agents and for detecting gastrointestinal
                                  are referred to as gastrointestinal defensin peptides. Comparison of the deduced AA sequences of the defensin S cDNA with the previously reported preprodefensisn shows significant similarity. The deduced AA sequence of defensin 6 cDNA has features similar to defensin 5 and the previously reported preprodefensins. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1993-405719/50.
                                                                                                                                                               ciones expressing new defensin related sequences were extensively characterised and found to contain genes selectively expressed in Paneth cells of the small intestin. These Paneth cell-derived defensins are designated human defensin 5 and human defensin 6 and
                                                                                                                                                                                                                                                                                                         A probe (D5' oligo) having the sequence given was used to screen a population of clones to i defensin peptides. Prof. the libraries were hu
                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                              disorders
                                                                                                                                                                                                                                              defensin peptides. Pref. the libraries were human genomic and cDNA libraries. Hybridisation and partial sequence analysis of the identified clones contained previously characterised myeloid derived defensin sequences as well as new defensin related sequences. Two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ę
                                                                                                                                                                                                                                                                                                                                                                                                   page 48-49; 97pp; English
                                                                                                                                                                                                                                                                                                                                          n in AAQ53219 (
identify novel
                                                                                                                                                                                                                                                                                                                                                           (claimed)
                                                                                                                                                                                                                                                                                                                                          defensin
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US-10-045-180A-4 (1-19) x AAQ53217 0.0419 64.00 89.47% 78.95% 71.11% (1-452)

Query Match:

Best Local Similarity:

Conservative: Mismatches: Indels:

0022145

Length: Matches:

Percent Similarity:

Alignment Scores:

No.:

Sequence 452

BP;

123 A;

118

C; 98

G; 113 T;

0

other;

19 1 MetArgThrLeuThrLeuSerAlaPheLeuSeuValAlaLeuGlnAlaTrpAla ATGAGAACCCTCACCATCCTCACTGCTGTTCTCCTCGTGGCCCTCCAGGCCAAGGCT 19

75

RESULT 7 ACA56600

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ACA56600 standard; 452

ACA56600;

06-JUN-2003 (first entry)

Human signalling pathway polynucleotide probe SEQ ID NO 1198.

Human; probe; 88; array element; Parkinson's disease; mmunopathy; ignalling pathway population; cancer; mmunopathy; AIDS; asthma; neuropathy; adenocarcinoma; leukaemia;

Homo sapiens

US6500938-B1

31-DEC-2002

30-JAN-1998; 98US-0016434

30-JAN-1998; 98US-0016434

(INCY-) INCYTE GENOMICS INC

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RESULT 8
AAT33496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a combination which, comprises a number of CC polynucleotide probes comprising a sequence selected from one of the 1490 CC sequences mentioned in the specification. The combination is useful as an CC array element in a microarray for monitoring the expression of a number CC of target polynucleotides. The microarray is particularly useful in the CC diagnosis and treatment of cancer and immunopathology and neuropathology. CC The microarray is useful in diagnostics and treatment regimens, drug CC discovery and development, toxicological and carcinogenicity studies, CC forensics and pharmacogenomics. The microarray is also useful for CC monitoring progression of diseases and for developing sophisticated CC profiles for the effects of currently available therapeutic drugs. The CC and genomic fragments and in research and diagnostic applications. The carray can detect changes in expression in a large number of genes coding for different signaling pathway populations which can be used to diagnose carray can detect changes in expression in a large number of genes coding for different signaling pathway populations which can be used to diagnose can detect changes in expression in a large number of sease coding conditions of the seases. The present sequence represents a polynucleotide control of the invention of the invention.
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Combination of polynucleotide probes, useful as array elements in a microarray for monitoring the expression of a number of target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probe of the invention.

Note: The sequence data for this patent did not form part of specification but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 1198; 65pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polynucleotides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 452 BP;
                                                                                                                                                                                                             Cationic peptide; CEMA; CEME; cecropia; melittin; bacterial growth; antibiotic activity; permeable; bacterial outer membrane;
                                                                                                                                                                                                                                                                                                         21-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                              AAT33496 standard; DNA; 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No.:
   13-MAR-1995;
                                                                       19-SEP-1996
                                                                                                          WO9628559-A1
                                                                                                                                                                                                                                                                       110mer used
                                   13-MAR-1996;
                                                                                                                                                                            intibiotic activity; permeable; bacterial outer membrane;
ipopolysaccharide; fusion peptide; inhibition; endotoxaemia;
sepsis associated disorder; septic shock; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seqdata.uspto.gov/sequence.html?DocID=06500938B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       19
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGAGAACCCTCACCATCCTCACTGCTGCTGCTCGTGGCCCTCCAGGCCAAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAla 19
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                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                       construction of pre pro cartridge.
                                   96WO-IB00431
   95US-0405234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.0419
64.00
89.47%
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Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
Gaps:
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coultured to express a fusion peptide comprising the cationic and anionic peptides. The biologically active cationic peptide is then recovered. The vectors constructed using theses sequences encode CEME, CEMA or HNP-1 (human neutrophil peptide 1). CEMA contains the first 18 amino acids of cecropin A and the last 8 residues of melittin. CEMA is derived from CC CEME by changing the C-terminal amino acid of CEME to include two cadditional Lys residues. This modification improves the antibiotic cativity of the peptide against many bacterial species, two fold, as well as substantially enhancing its ability to permeabilise bacterial membranes of the conjunction with antibiotics to permeabilise bacterial membranes breaking down the outer membrane conjunction with antibiotics to inhibit bacterial growth and to treat an endotoxaemia or sepsis can be considered to the context of the conte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oligonucleotides which were used in the construction of vectors used the method of the invention. The method comprises constructing an expression vector containing DNA encoding the cationic peptide adjace to DNA encoding an anionic carrier peptide which inhibits bacterial proteases. A bacterial host cell is transformed with the vector and anionic carrier peptide which the perton and the proteases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant production of antimicrobial, cationic peptide - produced in bacterial host as fusion peptide with an anionic portion for suppressing the anti-microbial activity of the cationic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequences given in AAT33488-500 and AAT40195-204 are oligonucleotides which were used in the construction of vectors used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Page 19; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYBR-) UNIV BRITISH COLUMBIA.
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CEMA or HNP-1 anionic

acent

S US-10-045-180A-4 (1-19) x AAT33496 (1-110) Query Match: Best Local Similarity: Score: Pred. No.: Percent Similarity: ,.. 0.025 61.00 84.21% 73.68% 67.78% Mismatches: Conservative: Indels: 1110 2 4 0

Sequence 110 BP; 21 A; 38 C; 32

G; 19

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0 other;

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AAT63059 standard; DNA; 110
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                                                                                                   MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAla 19
                                                                                 ATGAGGACCCTCGCCATCCTTGCTGCCATTCTCCTGGTGGCCCTGCAGGCCCAGGCT
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cecropin A; bee venom; melittin;
                                                                                                                                                                    25-MAR-2003
08-MAY-1997
                                                                Synthetic
                                                                                        permeability; antibiotic; E.
                                                                                                                         HNP-1; CEME;
                                                                                                                                              110-mer used
20-DEC-1995;
                     14-JAN-1997.
                                                                                        CEMA; human neutrophil protein; fusion; insect defensin; bee venom; melittin; antibiotic activity; S. typhimurium; betterial outer membrane; lipopolysaccharide; E. coli; Pseudomonas aeruginosa; E. cloacae; S. aureus; S
                                                                                                                                              in construction of pre pro cartridge.
                                                                                                                                                                    (updated)
(first en
 95US-0575052
                                                                                                                                                                     entry)
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WPI; 2001-483447/52
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20-DEC-1995;
20-DEC-1996;
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26-MAY-2000;
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03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                    Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABA75757;
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
                                                                                                                                                                                                                                                                                                                                  Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABA75757
                                                                                                                                                                                                                                                                                                                                                Score:
 Š
                                                                                                                                                                                                             The sequences given in AAT63051-64 represent oligonuclectides which were used in the construction of pGST-ppetide plasmids for the expression of HNP-1, CEME and CEMA. HNP-1 is peptide 1 from human neutrophil protein, CEME is a funion peptide made from portions of an insect defensin cercoin A and the bee venom peptide melittin, and CEMA is a variant of GEME with two additional lysine residues at the C-terminal end. The modification from CEME to CEME auses a two-fold improvement in antibiotic activity against many bacterial species as well as antibiotic activity against many bacterial species bacterial outer membranes and binding to lipopolysacharides. CEMA may be used synergistically with classical antibiotics to break down the outer membrane permeability barrier. It is possibly active against E. coli, Pseudomonas aeruginosa, E. cloacae, S. typhimurium and S. aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cecropin A; mellitin; CEME; fusion protein; polycationic; antibacterial; permeable; outer membrane; lipopolysaccharide; bacterial infection; septic shock; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAla 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                      of recombinant cationic peptide with antimicrobial activity form of a fusion peptide with protease-inhibiting anionic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGAGGACCTCGCCATCCTTGCTGCCATTCTCCTGGTGGCCCTGCAGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 110 BP; 21 A; 38 C; 32 G; 19 T; 0 other;
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Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                        Example 1; Columnm 9-10; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-045-180A-4 (1-19) x AAT63059 (1-110)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human pre-pro cartridge primer l.
                                                                                                                                      Prodn. of recombinant cationic in the form of a fusion peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV10895 standard; DNA; 110 BP.
                                                             (UYBR-) UNIV BRITISH COLUMBIA.
           93US-0110502.
92US-0933492.
95US-0575052.
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61.00
84.21%
73.68%
67.78%
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                                                                                      Hancock REW,
                                                                                                              WPI; 1997-099468/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
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             20-AUG-1993;
                       21-AUG-1992;
20-DEC-1995;
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21-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
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                                                                                      Brown MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
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                                                                                                                                                                peptide
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Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
                                                                                                                                                                                                                                                                                                                                                  production
                                                                                                                                                                                                                                                                                                                                        AAV10887-V10909 are primers used in a method which allows the productio of a novel polycationic antibacterial peptide, CEMA. This peptide is a 1s a hybrid comprising the first 18 amino acids of cecropin A and the last 8 amino acids of mellttin. It has two Lys residues at the C terminus which creates a sequence with two-fold increased antibiotic activity against many bacterial species as well as enhanced ability to permeabilise bacterial outer membranes and bind to lipopolysaccharide. CEMA can be used to treat bacterial infections and septic shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGAGGACCCTCGCCATCCTTGCTGCCATTCTCTCTGGTGGCCCTGCAGGCCCAGGCCT
                                                                                                                                                                                                                         - useful for treating bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human foetal liver single exon nucleic acid probe #24062.
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22
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                 Example 1; Column 10; 31pp; English.
                                                                                                                         Piers KL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                                        (UYBR-) UNIV BRITISH COLUMBIA.
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2000US-0632366.
2000US-0234687.
2000US-0236359.
95US-0575052.
96US-0770557.
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                                                                                                                                                                                                                      Antibacterial peptide CEMA infections and septic shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JAN-2001; 2001WO-US00669
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61.00
84.21$
73.68$
67.78$
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                                                                                                                         Brown MH, Hancock REW,
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                                                                                                                                                                     WPI; 1998-100348/09.
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Best Local Similarity:
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RESULT 13
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                                                                                                                                                                                                       Score:
      888888
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                                                                                                        The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAla 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGAGGACCCTCGCCATCCTTGCTGCTTCTCCTGGTGGCCCTGCAGGCCT
Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human bone marrow expressed single exon probe SEQ ID NO: 24955.
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                                                                 Claim 4; SEQ ID NO 24062; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                  Sequence 187 BP; 37 A; 60 C; 54 G; 36 T; 0 other;
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Mismatches:
Indels:
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Matches:
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26-MAY-2000; 2000US-0207456.
30-UUN-2000; 2000US-0608408.
33-UUN-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
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84.21%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-488900/53
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Best Local Similarit
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                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
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DB:
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bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAla 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, ds; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial diopathic pulmonary fibrosis; neurofibromatosis; tubercous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocyctosis; lymphangiolelomyomcosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dyshinesis; pulmonary dyshinesis; pulmonary hypertension; hypaline membrane disease; open reading frame; ORF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon probe ORF from lung SEQ ID No 23851.
                                                                                                                                                                                                                        187
22
3
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                                                                                                                                           Sequence 187 BP; 37 A; 60 C; 54 G; 36 T; 0 other;
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Matches:
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                                                                                                                                                                                                                                                                                                                                                      Gaps:
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2000US-234687P.
2000US-236359P.
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2000US-0608408
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84.21$
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                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
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26-MAY-2000; 2
30-JUN-2000; 2
03-AUG-2000; 2
21-SEP-2000; 2
27-SEP-2000; 2
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Pred. No.:
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DB:
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probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic acide expressed in the human lung; measuring the array with a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung comprising (a) algorithmically predicting at least one exon from genomic sequences of the array; identifying exons in a eukaryotic genome, comprising (c) having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single exon probe, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon in several caspove and (b) measuring the expression of each of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single exon in the probe are used for gene of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene of 12011 sequences, mentioned in the specification, or encoded by the cypobes/open reading frames (ORF). The probes are used for gene of 12011 sequences, mentioned in the specification, or encoded by the cypobes, interestitial lung disease (ILD), familial indiopathal and for the study of lung disease. (CODP), interestitial lung disease (ILD), familial lung disease (I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 187 BP; 37 A; 60 C; 54 G; 36 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probe open reading frame of the invention.
Note: The sequence data for this patent di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences.
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Length: Matches: Conservative: Mismatches: Indels: 61.00 84.21% 73.68% 67.78% Score:
Percent Similarity: Alignment Scores Query Match:

US-10-045-180A-4 (1-19) x ABS23860 (1-187)

Gaps:

MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAla 19 13 ATGAGGACCCTGGCCATCCTTGCTGCCATTCTCCTGGTGGCCCTGCAGGCCCAGGCT 69 ð

AAT26106 standard; cDNA to mRNA; 299 BP. RESULT 14 

(first entry) 18-OCT-1996

AAT26106;

Human gene signature HUMGS08342.

Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.

Homo sapiens

WO9514772-A1

94WO-JP01916. 11-NOV-1994;

93JP-0355504. 12-NOV-1993;

(MATS/) MATSUBARA K. (OKUB/) OKUBO K.

Matsubara K, Okubo

WPI; 1995-206931/27.

Identifying gene signatures in 3'-directed human cDNA library - for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human tissues

Claim 1; Page 2003; 2245pp; Japanese

A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences of given in AAT1901-T26837 and which is able to phybridise to part of human genomic DNA, cDNA or mANA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared C from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-entented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. C The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types. 

Sequence 299 BP; 67 A; 87 C; 83 G; 61 T; 1 other;

242800 94 Conservative: Mismatches: Length: Matches: Indels: Gaps: 61.00 84.21% 73.68% 67.78% Best Local Similarity: Percent Similarity: Alignment Scores: Pred. No.: Query Match:

US-10-045-180A-4 (1-19) x AAT26106 (1-299)

74 1 MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAla 19 셤

RESULT 15

AAF20911;

AAF20911 standard; DNA; 464 BP

(first entry) 14-MAR-2001

Human defensin 3 polynucleotide fragment #2478.

Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory, bronchodilator; antinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; crespiratory obstruction; pulmonary obstruction; impeded respiration; respiratory obstruction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pain; cystic fibrosis; allergic rhinitis; chronic obstructive pulmonary disease; pulmonary infection; bronchitis; cancer; 88 2X2X4X2X2X2X2X2X2X2XXXX

Homo sapiens.

WO200062736-A2

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26-OCT-2000.
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24-MAR-2000; 2000WO-US08020.

99US-0127958. 06-APR-1999;

(UYEC-) UNIV EAST CAROLINA. (NYCE/) NYCE J W.

Nyce JW;

WPI; 2000-679539/66.

Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions -

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense coligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with cartivating peptide factors and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, contral nervous system (CNS) and peripheral nervous and non-nervous system receptors, adenosine receptors, brandykninh receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (specially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy (ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vises principles (RP), pain, cystic fibrosis (CP), allergic rhinitis (AR), pulmonary transplantation rejection; pulmonary infections, bronchitis, and antisense oligonucleotides used in the exemplification of the present human polymodenties. Disclosure; Page 218; 1592pp; English the present invention. 

Sequence 464 BP; 110 A; 128 C; 119 G; 107 T; 0 other;

Conservative: Mismatches: Indels: Length: Matches: 0.146 61.00 84.21% 73.68% 67.78% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: DB:

US-10-045-180A-4 (1-19) x AAF20911 (1-464)

Search completed: December 17, 2003, 15:06:02 Job time : 72.25 secs

us-10-045-180a-4.rnpb

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Sequence 48280, A
Sequence 48281, A
Sequence 48281, A
Sequence 48284, A
Sequence 48280, A
Sequence 48280, A
Sequence 48281, A
Sequence 48283, A
Sequence 48283, A
Sequence 18938, A
Sequence 2522, App
                         Sequence 1, Appli
Sequence 1, Appli
Sequence 45, Appl
Sequence 45, Appl
Sequence 34, Appl
Sequence 34, Appl
Sequence 23, Appl
Sequence 13864, A
Sequence 16, Appl
Sequence 16, Appl
Sequence 78, Appl
Sequence 78, Appl
                                                                                                                                                                                                                                                                                                             252, App
8, Appli
141529,
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 473, App
Sequence 7, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/10013770
Publication No. US20020115151A1
GENERAL INFORMATION:
APPLICANT: GENSET SA
TITLE OF INVENTION: HUMAN DEFENSIN DEF-X GENE AND DNAC
TITLE OF INVENTION: HUMAN DEFENSIN CONTAINING SAME AND DIAGNOSTIC AND THERAPEUTIC APPLICANTONS
                                                                                                                                                                                                                                                                                                                                   Sequence 1
Sequence 1
Sequence 1
                                                                                                                                                                                                                                                                                                                                                                     Sequence 3
Sequence 3
Sequence 3
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COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                 US-09-816-828-16
US-10-125-237-78
US-10-105-891-78
US-10-105-891-78
US-10-027-632-48280
US-10-027-632-48281
US-10-027-632-181529
US-10-044-090-136
US-10-044-090-136
US-09-633-877-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-754-853A-1
US-10-027-632-247501
US-10-027-632-247501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSE: Knobbe, Martens, Olson & Bear STREET: 550 West C Street
CITY: San Diego
STATE: California
4 US-10-013-770-2
4 US-10-013-770-2
4 US-10-013-770-1
4 US-10-013-770-1
2 US-10-045-180A-1
2 US-10-367-169-45
3 US-10-367-169-34
3 US-10-367-169-34
3 US-10-076-802-34
1US-09-864-761-1864
3 US-09-864-761-1864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/013,770
   ZIP: 92101
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1375
684973
1182
  COUNTRY: USA
  US-10-013-770-2
  υo
                                                                                                                                                                                                                                                                                                                                                                                       Command line parameters:
-MODEL=frame+ p2n.model -DBV=xlp
-Q=/Cgnz_1/USPTO_spool_p/US10045180/runat_17122003_145026_12635/app_query.fasta_1.860
-Q=/Cgnz_1/USPTO_spool_p/US10045180/runat_17122003_145026_12635/app_query.fasta_1.860
-DB=Published Applications NA -OFMT=fastap -SUPFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOÖPEXT=0 -UNITS=bit s -START=1 -END=-1 -MATRIX=blosum62
-TRANS=humand-0.cdi -LIST=45 -DCALIGN=200 -THR MXS=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HERPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10045180 @CGN 1 1.174 @runat_17122003_145026_12635
-NCPU=6 -ICPU=3 -NO MMAP -LAGREQUERY NEG $CORSE=0 - WAIT -DSPBEACK=100
-LOOGLOG -DEV TIMEOUT=12 - WARN TIMEOUT=30 -THRRADS=1 -XGAPED=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                (without alignments)
963.776 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                    2003, 15:06:18 ; Search time 65.6915 Seconds
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'/ cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
'/ cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
'/ cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
'/ cgn2_6/ptodata/2/pubpna/DSO7_NEW_PUB.seq:*
'/ cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
'/ cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
'/ cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
'/ cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
'/ cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
'/ cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
'/ cgn2_6/ptodata/2/pubpna/USO0NEW_PUB.Seq:*
                                                                                                                                                                                                                                                                                   4423956
             GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                             nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                         2211978 segs, 1666101734 residues
                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published Applications NA:*
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                                                                                                                                                         MRTLTLLSAFLLVALQAWA 19
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Maximum DB seq length: 200000000
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90
1 MRTLTLLSAFLLVAI
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Match Length DB
                                                                                    December 17,
                                                                                                                                                                                   BLOSUM62
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                                                                                                                                              Perfect score:
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                                                             protein
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Sequence 1, Application US/10013770
Publication No. US20020115151A1
GENERAL INFORMATION:
APPLICANT: GENSET SA
TITLE OF INVENTION: HUMAN DEFENSIN DEF-X GENE AND DNAC
COMPOSITION CONTAINING SAME AND DIAGNOSTIC AND
THERAPEUTIC APPLICATIONS
                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/013,770
FILING DATE: 10-Dec-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSE: Knobbe, Martens, Olson & Bear STREET: 550 West C Street
CITY: San Diego
STATE: California
COUNTRY: USA
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 09/486,580
FILING DATE: cUnknown>
ATTORNEY/AGENT INPORMATION:
NAME: Hart, Daniel
REGISTRATION NUMBER: 40,637
REFERENCE/DOCKET NUMBER: GENSET.064C1
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: polyadenylation site
LOCATION: 4374..4379
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 4415 BASE PAIRS
TYPE: NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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1836..1874
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3394..3577
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4161..4380
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3406..3408
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4276..4278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: DOUBLE
TOPOLOGY: LINEAR
MOLECULE TYPE: DNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.05e-06
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NAME/KEY:
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LOCATION:
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Best Local Similarity:
Query Match:
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Pred. No.:
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                                                                                                                  US-10-013-770-1
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                                                                                                  RESULT 3
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; Bequence 2, Application US/10045180A
; Publication No. US20020182703A1
; GENERAL INFORMATION:
    APPLICANT: Bougueleret, Lydie
    APPLICANT: Chumakov, Ilya
    TITLE OF INVENTION: Human Defensin Polypeptide Def-X, Genomic DNA and cDNA, Compositi
    TITLE OF INVENTION: Containing Them and Applications to Diagnosis and to Therapeutic
    TITLE OF INVENTION NUMBER: US/10/045,180A
    CURRENT APPLICATION NUMBER: US 09/486,580
    PRIOR APPLICATION NUMBER: US 09/486,580
    PRIOR PILING DATE: 2000-02-25
    PRIOR APPLICATION NUMBER: FR 97/10823
    PRIOR PILING DATE: 1997-08-29
    RIOR FILING DATE: 1997-08-29
    NUMBER OF SEQ ID NOS: 12
    SOFTWARE: PatentIn Version 3.1
    SEQ ID NOS: 2
    TENNOR APPLICATION NUMBER: FR 97/10823
    PRIOR FILING DATE: 1997-08-29
    NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 ATGAGGACCCTCACCTCCTCTGCTTTCTCCTGGTGGCCCTTCAGGCCTGGGCA 108
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REGISTRATION NUMBER: 40,637
REGISTRATION NUMBER: 40,637
REPERENCE DOCKET NUMBER: GENSET.064C1
INFORMATION FOR SEG ID NO: 2:
SEQUENCE CHARACTERISTICS:
LINGTH: 453 BARE PAIRS
TYPE: NUCLEOTION TYPE: NUCLEOTION TYPE: TOPOLOGY: LINEAR MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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PILING DATE: 10-Dec-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/486,580
FILING DATE: «UNKNOWN.»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: CDS
; LOCATION: (52)..(336)
; OTHER INFORMATION: Def-X coding sequence
US-10-045-180A-2
                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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Best Local Similarity:
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Best Local Similarity;
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
Pred. No.:
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US-10-045-180A-2
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DB:
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NAME/KEY: misc feature
LOCATION: (4274)..(4276)
OTHER INFORMATION: Translation termination codon (TAA)
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NAME/KEY: misc_feature
LOCATION: (3406)...(3408)
FEATURE INFORMATION: Translation initiation codon (ATG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
LOCATION: (2710)..(2780)
OTHER INFORMATION: L1 fragment insertion
FEATURE:
NAME/KEY: misc_feature
LOCATION: (3391)..(3393)
OTHER INFORMATION: splice acceptor site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: misc_feature
LOCATION: (4161). (4163)
OTHER INFORMATION: splice acceptor site
                                                                                                                                             FEATURE:
NAME/KEY: misc feature
NAME/KEY: misc feature
NAME/KEY: misc feature
FEATURE:
NAME/KEY: misc feature
LOCATION: 0 = a, c, g, or t.
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NAME/KEY: misc_feature
LOCATION: (1875)..(1880)
OTHER INFORMATION: splice donor site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (3578)..(3583)
OTHER INFORMATION: splice donor site
FRATURE:
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LOCATION: (2155)..(2335)
OTHER INFORMATION: Alu insertion
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OTHER INFORMATION: n = a, c, g, FRATURE:
NAME/KEY: misc_feature
LOCATION: (2191)...(2191)
OTHER INFORMATION: n = a, c, g, FRATURE:
                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: misc_feature
LOCATION: (2133)..(2133)
OTHER INFORMATION: n = a, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (4123)...(4123)
OTHER INFORMATION: n = a, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (2367)..(2367)
OTHER INFORMATION: n = a,
  NAME/KEY: misc_feature
LOCATION: (1835)..(1874)
OTHER INFORMATION: Exon 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRATURE:
NAME/KEY: misc feature
LOCATION: (3394)..(3577)
OTHER INFORWATION: Exon 2
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LOCATION: (4164)..(4379)
OTHER INFORMATION: Exon 3
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NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                        RESULT 4

US-10-045-180A-1

i Sequence 1, Application US/10045180A

j Publication No. US20020182703A1

general INFORMATION:
APPLICANT:
APPLICANT:
Chumakov, Ilya

i TITLE OF INVENTION: Human Defensin Polypeptide Def-X, Genomic DNA and cDNA, Compositi

TITLE OF INVENTION: Human Defensin Polypeptide Def-X, Genomic DNA and cDNA, Compositi

TITLE OF INVENTION: Containing Them and Applications to Diagnosis and to Therapeutic
FILER REFERENCE: GEN-10001

CURRENT APPLICATION NUMBER: US/10/045,180A

CURRENT FILING DATE: 2001-10-18

PRIOR APPLICATION NUMBER: PCT/FF98/01864

PRIOR FILING DATE: 1999-08-28

PRIOR FILING DATE: 1999-08-29

NUMBER OF SEQ ID NOS: 12

SEQ ID NO 1

LENGTH: 4415
                                                                                                     3406 ATGAGGACCCTCACCTCTCTGTGCCTTTCTCCTGGTGGCCCTTCAGGCCTTGGGGCA 3462
                                                                               1 MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAla 19
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                                     US-10-045-180A-4 (1-19) x US-10-013-770-1 (1-4415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (1). (4415)
OTHER INFORMATION: Def-X genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: misc feature
LOCATION: (1780)...(1780)
OTHER INFORMATION: n = a, c, g, or t.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (1150)..(1150)
OTHER INFORMATION: n = a, c, g, or t.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (670)..(670)
OTHER INFORMATION: n = a, c, g, or
FEATURE:
NAME/KEY: misc feature
LOCATION: (970)..(970)
OTHER INFORMATION: n = a, c, g, or
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NAME/KEY: misc feature
LOCATION: (1111). (1111)
OTHER INFORMATION: n = a, c,
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NAME/KEY: misc_feature
LOCATION: (143)...(143)
OTHER_INFORMATION: n = a,
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LOCATION: (85)..(85)
OTHER INFORMATION: n = a,
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NAME/KEY: CAAT signal
LOCATION: (1711)..(1714)
OTHER INFORMATION:
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LOCATION: (1758)..(1767)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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SIGNAL SEQUENCES FOR POLYPEPTIDE EXPRESSION AND POLYPI
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US-10-076-802-34/c
is Sequence 34, Application US/10076802
is Deblication No. US20030162249A1
is GENERAL INFORMATION:
is APPLICANT: Gray, Jeff
APPLICANT: Buechler, Joe
is APPLICANT: Veeramallu, Uday K
ITILB OF INVENTION: EUKARYOTIC SIGNAL SEQUENCES FOR PROKARYOTIC EXPRESSION
FILLS REFERENCE: 014907-004700US
CURRENT APPLICATION NUMBER: US/10/076,802
CURRENT PILLING DATE: 2002-02-13
NUMBER OF SEQ ID NOS: 113
is SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                           1 MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAla 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 ATGCGTACTCTGGCTATCCTTGCAGCTATTCTGCTTGCACTGCAGGCTCAAGCG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: Primer EB US-10-367-169-34
                                                           ; OTHER INFORMATION: Neutrophil defensin 1,2,3 signal sequence US-10-076-802-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101
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Mismatches:
Indels:
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Mismatches:
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                                                                                                                                        Length:
Matches:
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Matches:
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US-10-367-169-34/C

Sequence 34, Application US/10367169

Sequence 34, Application US/10367169

Sequence 34, Application US/10367169

GENERAL INFORMATION:

APPLICANT: Gray, Jeff

APPLICANT: Buechler, Joe

APPLICANT: Veeramallu, Uday Kumar

TITLE OF INVENTION: BUCKARVOTIC SIGNAL SEQUENC

TITLE OF INVENTION: DISPLAY LIBRARIES

FILE REFERENCE: 11055US02

CURRENT APPLICATION WUMBER: 10/076,802

PRIOR APPLICATION NUMBER: 10/076,802

PRIOR FILING DATE: 2002-02-13

NUMBER OF SEQ ID NOS: 113

SOFTWARE: Patentin Ver: 2.1

SEQ ID NO 34

TYPE: DNA

CORTANIEN: Artificial Sequence
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61.00
84.21
73.68
67.78
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61.00
84.21%
73.68%
   TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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Pred. No.:
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US-10-367-169-45

US-10-367-169-45

Sequence 45, Application US/10367169

Publication No. US20030228660A1

GENERAL INFORMATION:
APPLICANT: Gray, Jeff
APPLICANT: Buechler, Joe
TITLE OF INVENTION:
TITLE OF INVENTION: DISPLAY LIBRARIES
TITLE OF INVENTION: DISPLAY LIBRARIES
FILE REPERBUCE: 11055US0.2

CURRENT APPLICATION NUMBER: US/10/367,169

CURRENT APPLICATION NUMBER: 10/076,802

PRIOR PLING DATE: 2002-02-13

NUMBER OF SEQ ID NOS: 113

SOFTWARE: Patentin Ver: 2.1

SEQ ID NO 45

LENGTH: 57
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i Sequence 45, Application US/10076802

i Publication No. US20030162249A1

i Publication No. US20030162249A1

i GENERAL INFORMATION:

APPLICANT: Buechler, Joe

APPLICANT: Wereamallu, Uday K

ITLE OF INVENTION: BUKARYOTIC SIGNAL SEQUENCES FOR PROKARYOTIC EXPRESSION

CURRENT APPLICATION UMBER: US/10/076,802

CURRENT FILING DATE: 2002-02-13

NUMBER OF SEQ ID NOS: 113

SOFTWARE PATENTING PATE: 2.002-02-13

SOFTWARE PATENTING PATE: 2.002-02-13

SOFTWARE PATENTING PATE: 2.002-02-13

SOFTWARE PATENTING PATE: 2.003-02-13

SOFTWARE STORMARE PATENTING PATE: 2.01

SOFTWARE STORMARE PATENTING PATE: 2.01

SOFTWARE STORMARE PATENTING PATE: 2.01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Neutrophil defensin 1,2,3 signal sequence US-10-367-169-45
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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90.00
100.00%
100.00%
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61.00
84.21%
73.68%
; LOCATION: (4374)..(4379)
; OTHER INFORMATION:
US-10-045-180A-1
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ORGANISM: Homo sapiens
                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
Query Match:
                                                                           Alignment Scores:
Pred. No.:
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1 MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAla 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAla 19
                                                                 FEATURE:
OTHER INFORMATION: MAP TO AF233439.1
OTHER INFORMATION: EXPRESED IN BONE MARROW, SIGNAL = 1.6e+02
OTHER INFORMATION: EXPRESED IN FETAL LIVER, SIGNAL = 18
OTHER INFORMATION: SEPRESED IN LUNG, SIGNAL = 24
OTHER INFORMATION: SWISSPROT HIT: P11479, EVALUE 7.00e-17
OTHER INFORMATION: BT HIT: X52053.1, EVALUE 1.00e-101
OTHER INFORMATION: EST_HUMAN HIT: AA321316.1, EVALUE 1.00e-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; FEATURE:
; NAME/KBY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030190640A1 903338.12
US-10-252-157-223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Pearse, Mary
APPLICANT: Pearsen, Cecelia I.
TITLEOP INVENTION: GENES EXPRESSED IN PROSTATE CANCER
FILE REPRENCE: PA-0027-1 US
CURRENT APPLICATION NUMBER: US/10/252,157
CURRENT FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: 60/295,048
PRIOR APPLICATION NUMBER: 60/295,048
PRIOR APPLICATION NUMBER: 50/295,048
SOFTWARE PERL PROGRAM
SOFTWARE PERL PROGRAM
SOFTWARE PERL PROGRAM
SEQ ID NOS: 501
SEQ ID NO 223
LENGTH: 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 7 7 7 8 0 0
1 4 8 0 0
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 31864
LENGTH: 187
                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
Indels:
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Sequence 15342 Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-252-157-223
; Sequence 223, Application US/10252157
; Publication No. US20030190640A1
; GENERAL INFORMATION:
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61.00
84.21%
73.68%
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61.00
84.21%
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ORGANISM: Homo sapiens
                                        TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
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Pred. No.:
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                                                                                                                                                                                                                                                                    77 ATGCGIACTCTGGCTATCCTTGCAGCTATTCTGCTTGTTGCACTGCAGGCTCAAGCG 21
                                                     FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Primer EE
                                                                                                                        101
14
2
3
3
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                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                        US-09-864-761-31864

. Sequence 31864, Application US/09864761

. Patent No. US20020048763A1

. GENERAL INFORMATION:
                        TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                        0.00658
61.00
84.21%
73.68%
67.78%
                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                             Alignment Scores:
Pred. No.:
                                                                                 US-10-076-802-34
SEQ ID NO 34
LENGTH: 101
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DB:
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241 ATGAGGACCCTGGCCATGCTGCTGCTTCTCCTGGTGGCCCTGCAGGCCCAGGCT 297
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                                                                                                                                                                                                 APPLICANT: Asundl, vincod
APPLICANT: Kei, Feiyan
APPLICANT: Xue, Aidong J.
APPLICANT: Wa, Yunqing
APPLICANT: Ma, Yunqing
APPLICANT: Mang, Zhiwei
APPLICANT: Zhao, Qinwei
APPLICANT: Zhao, Qinwei
APPLICANT: Zhao, Jian-Rui
APPLICANT: Brang, Jian-Rui
APPLICANT: Brang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: NUNERR: No'1/Peptides
FILE REFERENCR: 7910-122
CURRENT APPLICATION NUMBER: US/09/816,828
CURRENT APPLICATION NUMBER: 09/770,160
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 18
SOFTWARE: pt_F_genes Version 2.0
SEQ ID NO 16
LENGTH: 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20030022329Alel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 791CIP2ADIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       777800
77800
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Matches:
Conservative:
Mismatches:
Indels:
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                                          , Application US/09816828
US20020150898A1
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Publication No. US20030022329A1
GENERAL INFORMATION:
61.00
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Xue, Aidong J.
Zhang, Jie
Wehrman, Tom
Wang, Jian-Rui
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APPLICANT: Liu, Chenghua
APPLICANT: Zhou, Ping
APPLICANT: Asundi, Vinod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ren, Feiyan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: CDS
; LOCATION: (151)..(522)
US-09-816-828-16
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Best Local Similarity:
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US-10-125-237-78
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APPLICANT:
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                                                            APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: MAP TO AF233439.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6e+02
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 18
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 24
                                                                                                                                                                                                                         UCKKENI FILLING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILLING DATE: 2000-02-04
PRIOR FILLING DATE: 2000-05-26
PRIOR FILLING DATE: 2000-08-03
PRIOR FILLING DATE: 2000-08-03
PRIOR FILLING DATE: 2000-08-03
PRIOR FILLING DATE: 2000-09-04
PRIOR PLILING DATE: 2000-09-04
PRIOR FILLING DATE: 2000-09-07
PRIOR FILLING DATE: 2000-09-07
PRIOR FILLING DATE: 2000-09-07
PRIOR FILLING DATE: 2001-01-30
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2001-01-29
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01
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                                       Rank, David R.
Hanzel, David K.
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ORGANISM: Homo sapiens
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CURRENT APPLICATION NUMBER: US/10/125,237
CURRENT FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 09/659,317
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 09/552,929

RESULT 12 US-09-816-828-16

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GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Abou, Ping
APPLICANT: Zhou, Ping
APPLICANT: Zhou, Ping
APPLICANT: Zhou, Ping
APPLICANT: Ren, Felyan
APPLICANT: Zhou, Qing A.
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Wehrman, 100
APPLICANT: Dramanac, Radio, Tille OF INVENTION WHORER: US/10/105,891
CURRENT APPLICATION WHORER: 09/668,317
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PF_Genes Version 2.0
ENGTH: LANGTH: 1348
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Matches:
Conservative:
Mismatches:
Indels:
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Conservative:
Mismatches:
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US-10-105-891-78
; Sequence 78, Application US/10105891
; Publication No. US20030073099A1
; GENERAL INFORMATION:
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 91
SOFTWARE: Pt_Ft_genes Version 2.0
SEQ ID NO 78
LENGTH: 1348
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-10-125-237-78
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US-10-105-891-78
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Sequence:

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US-09-486-580A-2

Sequence 2, Application US/09486580A

Patent No. 632914

TITLE OF INVENTION:

APPLICANT GENSET SA

TITLE OF INVENTION: HUMAN DEFENSIN DEF-X GENE AND DIAGNOSTIC AND TITLE OF INVENTION: THERAPEUTIC APPLICATIONS

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE:

ADDRESSEE:

ADDRESSEE:

ADDRESSEE:

ADDRESSEE:

CONTRY:

San Diego

SITTS:

CONTRY:

MEDIUM TYPE: Floppy disk

CONPUTER: DAN FC compatible

CONPUTER: THE PRICATION DATA:

APPLICATION NUMBER: US/09/486,580A

ATILING DATE: FERRIARY 25, 2000

ATTORNEY/AGENT INFORMATION:

NAME: Hart, Daniel

RESERRACE/DOCKET NUMBER: 40,637

REFERRACE/DOCKET NUMBER: 40,637

REFERRACE/DOC
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US-08-725-160-5

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US-08-725-12

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US-08-770-52-12

US-08-770-52-12

US-08-770-52-12

US-08-770-52-12

US-08-90-402-01-44

US-08-90-402-01-44

US-08-90-913-66

US-08-90-913-66

US-08-482-279-66

US-08-482-279-66

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US-08-482-279-66

US-08-482-279-69

US-08-482-279-69

US-08-482-279-69

US-08-482-279-69

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US-08-342-268-69

US-08-342-383-5

US-08-423-383-5

US-08-486-013-488

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-DE=ISSUEd_PSTO spool_p/USIO045180/runat 17122003_145024_12553/app_query.fasta_1.860
-DE=ISSUEd_PSTO spool_p/USIO045180 -SUFFIX=rni -MINMATCH=0_1 -LOOPCL=0
-LOOPEXT=0 -UNITS-Dits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL_OUTFNT=pto -NORM=ext -HARPSIZE=500 -MINIENE - MAXLEN=200000000
-USER=USIO045180 @CGN 1 1.93 @runat 17122003 145024 12553 -NCFU=6 -ICFU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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441.383 Million cell updates/sec
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2: /cgn2_6/ptcdata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptcdata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptcdata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptcdata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptcdata/2/ina/PCTUS_COMB.seq:*
                        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                             nucleic search, using frame plus p2n model
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US-09-486-580A-1
US-08-158-189-6
US-08-158-189-9
US-08-158-189-9
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US-08-775-55-9
US-08-770-557-9
US-08-770-557-9
US-08-405-214-9
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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Maximum DB seq length: 2000000000
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Perfect score:
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US-10-045-180A-4 (1-19) x US-08-158-189-6 (1-452)
 ; LOCATION:
US-09-486-580A-1
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ZIF: 92101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/486,580A
FILING DATE: FERRUARY 25, 2000
ATTORNEY/AGENT INFORMATION:
NAME: Hart, Daniel:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
ILENGTH: 4415 BASE PAIRS
TYPE: NUCLEOTIDE
STRANDENESS: DOUBLE
TOPOLOGY: LINEAR
MOLECULE TYPE: DNA
MORGANISM: HOMO sapiens
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Matches:
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; ORGANISM: Homo sapiens
US-09-486-580A-2
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US-09-486-580A-1
                                                              Pred. No.:
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US-08-158-189-6

Sequence 6, Application US/08158189

Patent No. 5641497

Patent No. 5641497

GENERAL INFORMATION:

APPLICANT: Bevins, Charles L.

APPLICANT: Bevins, Charles L.

APPLICANT: Bevins, Charles L.

TITLE OF INVENTION: Gastrointestinal Defensin Peptides,

TITLE OF INVENTION: GASTROINTESTINAL SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSED: Woodcock Washburn Kurtz Mackiewicz and No. 5641497ris

STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3406 ATGAGGACCCTCACCTCTCTGCCTTTCTCCTGGTGGCCCTTCAGGCCTTGAGGA 3462
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/158,189
FILING DATE:
APPLICATION NUMBER: US/07/888,232
RIGHT APPLICATION DATA:
APPLICATION NUMBER: US/07/888,232
FILING DATE:
APPLICATION NUMBER: US/07/888,232
FILING DATE:
APPLICATION NUMBER: 27,200
REGISTRATION NUMBER: 215-568-3100
TELECOMMUNICATION INFORMATION:
TELEFRONE: 215-568-3109
THOOMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LEMGTH: 452 Dase pairs
TUBETH TEMETER TOWN: LEMGTH TOWN: L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            446
23
20
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                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                      5.33e-06
90.00
100.00%
100.00%
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64.00
89.47$
78.95$
71.11$
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TYPE: nucleic acid
STRANDEDNESS: single
4374..4379
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US-08-158-189-6
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                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: PA
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 19103
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                                                                                                        Alignment Scores:
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ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 195 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.00641
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84.21%
78.95%
70.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown US-08-158-189-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
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Pred. No.:
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                     MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAla 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAla 19
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                                                                                                       Sequence 1198, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Jaffrey J. Seilhamer
ITILE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
VUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSEE: INC.
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP. 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKGT NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEFAX: (650) 845-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1198:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
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APPLICANT: Bevins, Charles L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.00
89.47%
78.95%
71.11%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 452 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                     CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LIBRARY: GENBAN
; CLONE: 9181546
US-09-016-434-1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity:
                                                                      RESULT 4
US-09-016-434-1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
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US-08-158-189-9
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Score:

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Douglas E.
Gastrointestinal Defensin Peptides,
cDNA Sequences, Methods for Production and Use Thereof
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Sequence 8, Application US/08158189

Sequence 8, Application US/08158189

Patent No. 5641497

PAPELICANT: Bevins, Charles L.

APPLICANT: Bevins, Charles E.

TITLE OF INVENTION: Gastrointestinal Defensin Peptides,

TITLE OF INVENTION: CDNA Sequences, Methods for Production and Use Thereof

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 ATGAGGACCCTGCTCTGCTTGCTGCCATTCTCCTGGTGGCCCTGCAGGCCCAGGCT 126
APPLICANT: Jones, Douglas E.
TITLE OF INVENTION: Gastrointestinal Defensin Peptides,
TITLE OF INVENTION: Gastrointestinal Defensin Peptides,
NUMBER OF INVENTION: CDNA Sequences, Methods for Production and Use
NUMBER OF SEQUENCES: 51
CORRESSONDMESS:
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz and No. 5641497ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAla
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STREET: One Liberty Place - 46th.Floor
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                       CUDNIEKY: U.S.A.

ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
GUFRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/158,189
FILING DATE:
CLASSIFICATION: A35
FILING DATE:
APPLICATION NUMBER: US/07/888,232
FILING DATE:
APPLICATION NUMBER: US/07/888,232
FILING DATE:
APPLICATION NUMBER: US/07/888,232
FILING DATE:
ATFORNEY/AGENT INFORMATION:
NAME: Johnson, Philip S.
REGISTRATION NUMBER: 27,200
REFERENCE/DOCKET NUMBER: 27,200
REFERENCE/DOCKET NUMBER: CH-0219
TELEFHONE: 215-568-3100
TELEFHONE: 215-568-3109
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Mismatches:
Indels:
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Matches:
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TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 61.00
84.21%
73.68%
67.78%
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U
ZIP: 92037
                                                                                                                                                                                                                                           , NAME/KEY:
, LOCATION:
US-08-575-052-9
                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
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US-08-614-516A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                           red. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                       score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 AIGAGGACCCTCGCTCTGCTTGCTGCCATTCTCCTGGTGGCCCTGCAGGCT 133
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US-08-575-052-9
US-08-575-052-9
Sequence 9, Application US/08575052
Fatent No. 5593866
GENERAL INFORMATION:
APPLICANT: HANCOCK, ROBERT E.W.
APPLICANT: HANCOCK, ROBERT E.W.
APPLICANT: BROWN, MELISSA H.
ITTLE OF INVENTION: CATIONIC PEPTIDES AND METHOD FOR PRODUCTION NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 90067
COMPUTER: IBM PC COMPALIBLE
SOFTWARE: PATELIAN RELEASE #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/575,052
FILING DATE:
FILI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202
115
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/158,189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-045-180A-4 (1-19) x US-08-158-189-8 (1-202)
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Gaps:
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/110,502
FILING DATE: 20-AuG-1993
ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, UR., PH.D., JOHN R.
REGISTRATION NUMBER: 31,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/455-5100
TELEPHONE: 619/455-5100
                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,232
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Johnson, Philip S.
REGISTRATION NUMBER: 27,200
REFERENCE/DOCKET NUMBER: CH-0219
TELEPHONE: 215-568-3100
TELEPAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 202 base pairs
TYPE: nucleic acid
STRANDENNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.00669
63.00
84.21%
78.95%
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Pred. No.:
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DB:
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APPLICANT: HANCOCK, ROBERT E.W.
APPLICANT: PIERS, KEVIN I.
APPLICANT: BROWN, MELISSA H.
APPLICANT: BROWN, MELISSA H.
APPLICANT: REALY, MIAMH
TITLE OF INVENTION: TREATMENT OF ENDOTOXIN-ASSOCIATED
TITLE OF INVENTION: DISORDERS WITH CATIONIC PEPTIDES
TITLE OF INVENTION: DISORDERS WITH CATIONIC PEPTIDES
OFRESPONDENCE ADDRESS:
ADDRESSEE: FISH & RICHARDSON P.C.
STREET: 1425 Executive Square, Ste. 1400
CITY: La Johla
STATE: CALIFORNIA
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/614,516A
FILING DATE: 13-MAR-1996
CLASSIPICATION: 435
ATTONEY/AGENT INFORMATION:
NAME: HALLE, PH.D., LISA A.
REGISTRATION NUMBER: 38.347
REFERENCE/DOCKET NUMBER: 07420/010001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 9:
INFORMATION FOR EQ ID NO: 9:
LENGTH: 110 base pairs
TUBNGTH: 110 base pairs
Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                           US-10-045-180A-4 (1-19) x US-08-575-052-9 (1-110)
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Patent No. 5688767
GENERAL INFORMATION:
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1 MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAla 19
                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                            5 ATGAGGACCCTCGCCATCCTTGCTGCCATTCTCCCTGGTGGCCCTGCAGGCCTAGGTGCCAGGCT
                                                                                                                                                                                                                                                                                                                                       RESULT 9
US-08-770-557-9
US-08-770-557-9
Sequence 9, Application US/08770557
Patent No. 5707855
GENERAL INFORMATION:
APPLICANT: HANOCK, ROBERT E.W.
APPLICANT: BROWN, MELISSA H.
TILE OF INVENTION: CATIONIC PEPTIDES AND METHOD FOR PRODUCTION TUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 9006 COMPUTER: FLODEY disk
COMPUTER: READABLE FORM:
MEDIUM TYRE: 18M PC COMPATIBLE
COMPUTER: 20-BC-1996
CLASSIFICATION NUMBER: US/08/110,502
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,678
ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, UR., PH.D., JOHN R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD2823
TELECOMMUNICATION NUMBER: PD2823
TELECOMMUNICATION NUMBER: BD2823
TELEFRAMIS DASSES: S1106
SEQUENCE CHARACTERISTICS:
LENGTH: 110 Dase Pairs
TTREE NUCLEIC acid
SEQUENCE THARACTERISTICS:
LENGTH: 110 Dase Pairs
TTREE NUCLEIC ACID
                    Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Matches:
Conservative:
Mismatches:
Indels:
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84.21$
73.68$
67.78$
                                              61.00
84.21%
73.68%
67.78%
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; LOCATION: 2..110
US-08-770-557-9
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Best Local Similarity:
Query Match:
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Query Match:
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Alignment Scores:
Pred. No.:
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JS-10-045-180A-4 (1-19) x US-08-770-557-9 (1-110)

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INFORMATION FOR SEQ ID NO: 38:
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Patent No. 5641497
GENERAL INFORMATION:
APPLICANT: Bevins, Charles L.
APPLICANT: Jones, Douglas E.
TITLE OF INVENTION: Gastrointestinal Defensin Peptides,
TITLE OF INVENTION: CDNA Sequences, Methods for Production and Use Thereof
Gastrointestinal Defensin Peptides, cDNA Sequences, Methods for Production and Use Thereof
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CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz and No. 5641497ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                    NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz and No. 5641497ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                            COUNTRY: U.S.A.

ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/158,189
FILING DATE:
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COUNTRY: U.S.A.
ZIP: 1910.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,232
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Johnson, Philip S.
REGISTRATION NUMBER: 27,200
REFERENCE/DOCKET: NUMBER: CH-0219
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 203 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.00
84.21%
73.68%
67.78%
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TITLE OF INVENTION:
TITLE OF INVENTION:
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Query Match:
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                                                                                                                                            STATE: PA
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US-08-158-189-11
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CURRENT APPLICATION DATA:

PRICATION MORRER: US/09/159,189

CLASSICDATION:

PRICATION MORRER: US/07/864,232

CLASSICDATION:

PRICATION WORKER: US/07/864,232

PRICATION WORKER: US/07/864,232

PRICATION WORKER: US/07/864,232

PRICATION WORKER: US/07/864,232

PRICATION WORKER: US/07/864,130

PREPARENCE/DOCKER WORKER: US/07/86
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1 MetArgThrLeuThrLeuLeuSerAlaPheLeuLeuValAlaLeuGlnAlaTrpAla 19
                                                                                                                                     10 ATGAGGACCATCGCCATCCTTGCTGCTGCTGCTGGTGGCCCTGCAGGCCCAGGCT 66
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                                                                                       RESULT 15

US-08-021-608D-5/C

S SQUENCE 5. APPLICATION US/08021608D

PATCH NO. 5580760

GENERAL INFORMATION:
APPLICANT: LEVENS, DAVID L., DUNCAN,
APPLICANT: ROBERTC, AND AVIGAN, MARK I.
TITLE OF INVENTION: PROTEIN AND CDNA THEREPOR
TITLE OF INVENTION: PROTEIN AND CDNA THEREPOR
TITLE OF INVENTION: PROTEIN AND CDNA THEREPOR
MUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSED: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
COUNTRY: USA
ZIP: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                     US-10-045-180A-4 (1-19) x US-08-158-189-4 (1-424)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
ATORNEY AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYBE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/021,608D
FILING DATE: 22-FEB-1993
CLASSIFICATION: 435
PRIOR APPLICATION 0474:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.252
59.00
88.24%
76.47%
65.56%
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STRANDEDNESS: Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity:
Query Match:
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Pred. No.:
        Query Match:
DB:
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Patent No. 5641497
GENERAL INFORMATION:

APPLICANT: Bevins, Charles L.
APPLICANT: Jones, Douglas E.
TITLE OF INVENTION: Gastrointestinal Defensin Peptides,
TITLE OF INVENTION: CDN Sequences, Methods for Production and Use Thereof
NUMBER OF SEQUENCES: 5:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5641497ris
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                     34 ATGAGGACCTCGCCATCCTTGCTGCCATTCTCCTGGTGGCCCTGCAGGCCCAGGCT 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/158,189
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Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Johnson, Philip S.
REGISTRATION NUMBER: 27, 200
REFERENCE DOCKET NUMBER: 27, 200
REFERENCE DOCKET NUMBER: CH-0219
TELEPAN: 215-568-3100
TELEFAN: 215-568-3439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 424 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,232
FILING DATE:
SEQUENCE CHARACTERISTICS:
FINGTH: 218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLIGY: unknown
US-08-158-189-38
                                                                                                                                                                      0.0163
61.00
84.21%
73.68%
67.78%
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84.21$
68.42$
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; LOCATION: 10..294
US-08-158-189-4
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Best Local Similarity:
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Best Local Similarity:
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COUNTRY: U.
ZIP: 19103
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Search completed: December 17, 2003, 14:54:00 Job time : 20 secs

Run on:

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AX40593 Sequence
U33317 Human defen
AC021883 Homo sapi
AR181803 Sequence
AX047114 Sequence
AK047114 Sequence
AK184156 Macaca mu
AR181796 Sequence
AX047101 Sequence
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AX047111 Sequence
AX047111 Sequence
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AF314060 Homo sapi
AF231439 Homo sapi
AF200455 Homo sapi
AF205406 Homo sapi
AF355799 Homo sapi
AR270635 Sequence
149588 Sequence
M98331 Homo sapien
AF314059 Homo sapien
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U10267 Human defen
AF144257 Homo sapien
U108745 Human corti
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BD074746 Human def
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BD074745 Human def
AF238378 Homo sapi
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M23281 Human defen
X13621 Human HNP-3
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                                                                                                                                                                                                                                                                                                  Description
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AF184157
RABDNP3AB
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AF184158
AR181795
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AF191100
I49587
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AC079018
AF205406
AF355799
AR270635
I49588
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AR181796
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BD074745
AF238378
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AC021883
AR181803
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AF104257
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AX405993
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AR181800
HUMDEF1A
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89.7 4415
86.3 128544
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77.7 188604
48.9 542
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46.4 4580
46.4 79730
46.4 158653
46.4 168702
46.4 168702
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-MODELETRAND - DEVEXID
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1 EPLQARAHEMPAQKQPPADD.....IYFSGDDSCSLQVPGSTKGL 44
             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                  OM protein - nucleic search, using frame_plus_p2n model
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Maximum Match 100%
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Fgapop 6.0 , Fgapext
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Bougueleret, L. and Chumakov, I.

HUMAN DEFENSIN DEF-X, GENE AND DNAC, COMPOSITION CONTAINING SAME
HUMAN DEFENSIN DEF-X, HERREPEUTIC APPLICATIONS
PATENT: WO 9911663-A 1 11-MRA-1999;
BOUGUELERET LYDIE (FR); CHUMAKOV LIYA (FR)
                                                                                                                                                           containing the same, and application to diagnosis and remedy
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Human defensin polypeptide Def-X, genome DNA and cDNA, composition
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C12P21/02,
PC C12P21/08,C12Q1/68,G01N33/53,A61K37/02,C12N15/00
Strandedness: Double;
CC Topology: Linear;
CC Human defensin polypeptide Def-X, genome DNA and
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Human defensin polypeptide Def-X, genome DNA and cDNA, composition containing the same, and application to diagnosis and remedy treatment.

BD074746

BD074746

JD 2001514264-A/2.

Homo sapiens (human)
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1 (bases 1 to 453)

Bougueleret, L. and Shmacov, I.
Human defensin polypeptide Def.X, genome DNA and cDNA, composition containing the same, and application to diagnosis and remedy GRNSET.
                               PAT 26-JAN-2000
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JP 2001514264-A/2
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11-SEP-2001
29-AUG-1999 JP 2000508701
29-AUG-1997 FR 97/10823
LYDIE BOUGUELERET, 1LYA SHMACOV
COTKILAS, A01N43/50, A01N63/00, A61K7/00, A61K38/00, A61P29/00, A61P35/00, 
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Bougueleret, L. and Chumakov, I.

HUMAN DEFENSIN DEF-X, GENE AND DNAC, COMPOSITION CONTAINING SAME
HUMAN DISCRICT AND THERAPETIC APPLICATIONS
PATENT: WO 9911663-A 2 11-MAR-1999;

BOUGUELERET LYDIE (FR); CHUMAKOV ILYA (FR)
LOCATION/Qualifiers
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121 c 97 g 121
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1 (bases 1 to 4415)

1 sougueleret,L. and Shmacov,I. Human defensin polypeptide Defex, genome DNA and cDNA, composition containing the same, and application to diagnosis and remedy Patent: JP 2001514264-A 1 11-SEP-2001;
                                                                                                                                                                                                                BD074745

Human defensin polypeptide Def-X, genome DNA and cDNA, composition containing the same, and application to diagnosis and remedy
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A61P37/02,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N15/09, PC
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Human defensin polypeptide Def-X, genome DNA and cDNA,
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Mismatches:
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JP 2001514264-A/1
11-SEP-2001
28-AUG-1998 JP 2000508701
29-AUG-1997 FR 97/10823
LYDIE BOUGUELERET, ILYA SHWACOV
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/mol type="qenomic DNA"
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3406. .3408
4276. .4278.
Location/Qualifiers
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3394. .3577
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JP 2001514264-A/1.
Homo sapiens (human)
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PD IJ-SEP-2001
PP 28-AUG-1998 JP 200
PR 29-AUG-1997 FR
PI LYDIB BOUGUBLERET,
PC COYKI4/A35,A01N43,PC A61P35/00,
PC A61P37/02,CO7K16/J
PC C12P21/02,
PC C12P21/08,C12Q1/68
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VERSION
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TITLE
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US-10-045-180A-5 (1-44) x BD074745 (1-4415)

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Direct Submitted (10-MOV-2000) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany Chases 1 to 128544)

S foases 1 to 128544)

L Submitted (10-MUL-2002) Genome Analysis, Institute of Molecular Submitted (06-UUL-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany G (Dases 1 to 128544)

E Genamn, D. and Platzer, M. Direct Submission Direct Submission Direct Submission Direct Submission Direct Submission Direct Submission Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany On Apr 2, 2003 this sequence version replaced gi:21700555.
                                                                                                                                                                                                                                                                                                 AFZ18378 128544 bp DNA linear PRI 02-APR-2003
Homo sapiens chromosome 8 clone SCD-561b17 map p22-p21, complete
sequence.
3463 GAGCCGCTCCAGGCAAGAGCTCATGAGATGCCAGCCAGCAGCAGCTCCAGCAGTGAC 3522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 12854)

Polley, A., Baumgart, C., Blechschmidt, K., Dette, M.D., Jahn, N., Menzel, U., Reichwald, K., Schilhabel, M.B., Schudy, A., Taudien, S., Wen, G., Schutte, B., Malik, M., Peng, J. Hong., McCray, P. and Chromosome 8 genomic sequence

Unpublished
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3 (bases 1 to 128544)
5 (bases 1 to 128544)
6 Genome Sequencing Center Jena.
Direct Submission
Submitted (24-MAY-2000) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany Genome Sequencing Center Jena.
Direct Submission
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                                                                                                          21 GlnAspValVallleTyrPheSerGlyAspAspSerCysSerLeuGlnValProGly 39
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Direct Submission
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Center project Information
Center clone name: 830-561b17
Center clone name: 830-561b17
Center clone name: 800-561b17
Sequencing vector: pUC18; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 127999 bases at least Q40
Consensus quality: 128930 bases at least Q30
Consensus quality: 128544 bases at least Q20
Quality coverage: 11.05x
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Contact: gscj-submit@genome.imb-jena.de
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Homo sapiens
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/note="single stranded/single chemistry region"
61859 .61859
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/note="single stranded/single chemistry region"
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'note="single stranded/single chemistry region"
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 This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                  Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part
of this entry's ASN.1 file.
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15815. .45872
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7899. .47900
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1. .188604
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89.74$
77.68$
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Best Local Similarity:
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                                                                            AC116559 163093 bp DNA linear HTG 30-MAY-2003
Papio anubis clone rp41-339c10, WORKING DRAFT SEQUENCE, 3 ordered
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1. (Dases 1 to 163093)

Xu, W., Hua, A., Eichler, E. and Roe, B.A.
Papio anubis BAC Clone rp41-339c10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (39-MAR-2002) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
3 (bases I to 163193)
Xu, W., Hua, A., Eichler, E. and Roe, B.A.
Direct Submission
Submitted (30-MAY-2003) Department Of Chemistry And Biochemistry, And Markey of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                             63206 CAGGATGTGGTCCTTTACTTTTCAGGAGATGACAGCTGCTCTTCAGGTTCCAGGT 63150
                                                          1 GluProLeuGlnAlaArgAlaHisGluMetProAlaGlnLysGlnProProAlaAspAsp 20
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/clone lib="RPCI - 41 Male (Olive) Baboon BAC Library"
36508 c 35861 g 46065 t 224 others
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* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* 6315 contig of 6315 bp in length 6415: gap of unknown length 6416 16704: contig of 10289 bp in length 6416 16805 163093: contig of 146289 bp in length.
                                                                                                                             21 GlnAspValValI1eTyrPheSerGlyAspAspSerCysSerLeuGlnValProGly 39
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35
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/organism="Papio anubis"
                      US-10-045-180A-5 (1-44) x AF238378 (1-128544)
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/db xref="taxon:9555"
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HTG; HTGS PHASE2; HTGS DRAFT.
Papio anubis (olive baboon)
Papio anubis
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Dupublished

Z (bases 1 to 188604)

S Xu,W., Hua,A., Eichler,E. and Roe,B.A.

Direct Submission

I Submitted (29-MAR-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA

Xu,W., Hua,A., Eichler,E. and Roe,B.A.

S Xu,W., Hua,A., Eichler,E. and Roe,B.A.

I Submitted (11-UNN-2003) Department Of Chemistry And Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA

On May 15, 2003 this sequence version replaced gi:28173120.
                                                                                                                                                                                                                                             32923 GAGCCGCTCCAGGCAAGAGCTGATGAGATGCCAGGAGCAGGAGCAGCTCCAGGAAACGAC 32982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC116558 11-JUN-2003
Papio anubis clone rp41-273g19, WORKING DRAFT SEQUENCE, 2 ordered
                                                                                                                                                                                                                 1 GluProLeuGlnAlaArgAlaHisGluMetProAlaGlnLysGlnProProAlaAspAsp 20
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Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae;
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/clone lib="RPCI - 41 Male (Olive) Baboon BAC Library"
53384 a 41769 c 40796 g 52555 t 100 others
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* This sequence will be replaced

* by the finished sequence as soon as it is available and the accession number will be preserved.

* the accession number will be preserved.

* 6059: contig of 6057 bp in length

* 6158 188664 contig of 182447 bp in length.
                                                                                                                                                                                                                                                                                                                                     21 GlnAspValValIleTyrPheSerGlyAspAspAspSerCysSerLeuGlnValProGly 39
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Conservative:
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1 (bases 1 to 188604).
Xu,W., Hua,A., Eichler E. and Roe,B.A.
Papio anubis BAC Clone rp41-273g19
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/db xref="taxon:9555"
                                                                                          Gaps:
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AC116558.16 GI:30725961
HTG; HTGS PHASE2; HTGS DRAFT.
Papio anubis (olive baboon)
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Alignment Scores:

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Homo sapiens (human)

Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 4580)

Bevins, C.L. and Jones, D.E.

Analysis of the Human Defensin Gene Locus: Sequence of Clone HG27B

Unpublished

2 (bases 1 to 4580)

Es Bevins, C.L. and Jones, D.E.

Bevins, C.L. and Jones, D.E.

Is Evins (L. and Jones, D.E.

Direct Submission

N. Submitted (15-007-1999) Immunology, The Cleveland Clinic

Foundation, 9500 Euclid Avenue, Cleveland, OH 44195, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRI 09-DEC-1999
                                                                                                                                                                          GlnAspValVallleTyrPheSerGlyAspAspSerCysSerLeuGlnValProGlySer 40
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1. 1175 c. 950 g. 1261 t.
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Matches:
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46.35%
               3.46e-07
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232 AGGGGCATG 240
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                                                                                                                                                                                                                                                                                                 PRI 07-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 52)
Palfree, R.G., Sadro, L.C. and Solomon, S.
The gene encoding the human corticostatin HP-4 precursor contains recent 86-base duplication and is located on chromosome 8 Mol. Endocrinol. 7 (2), 199-205 (1993)
                                                                                                                                                                                                                          142549 CAAGATGTGGTCATTTACTTTTTCAGGAGATGACAGCTCCTCTTCAGGTTCCAGGT 142493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (05-MAY-1992) R.G.E. Palfree, McGill University Royal
Victoria Hosp., Rm L2.05, 687 Pine Ave West, Montreal PQ, H3A LA1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="recent duplication of immediate upstream segment"
137 c 135 g 152 t
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1. .542
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H.sapiens mRNA for corticostatin HP-4 precursor.
X65977
    188604
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corticostatin/defensin.
Homo sapiens (human)
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Palfree, R.G.E.
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BI021150 CM0-MT035 BX099382 BX099382

Description

AI082774 ox74a06.x AA722853 zg85h07.s AI250799 qi36g07.x

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BI021150 307 bp mRNA linear EST 14-JUN-2001 CMO-MT0351-150101-736-b03 MT0351 Homo sapiens cDNA, mRNA sequence.
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                       SUMMARIES
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BM830493
BM855729
BM855729
BM855729
BM855276
BM855276
BM855593
BM708419
BM70851315
BM715953
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AA321102
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gb_gss2:*
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DEFINITION
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BI021150/c
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-MODEL=frame+ p2n.model -DEV=xlp
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-D=/COR_2 1/USPTO_spool p/US10045180/runat 17122003 145024 12540/app_query.fasta_1.860
-D=/COR_2 1/USPTO_spool p/US10045180/runat 17122003 145024 12540/app_query.fasta_1.860
-DEST -QFWT=fastap -SUPFTX=rst -MINNATCH=0.1 -LOOPELMO -LLOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIA-blosume2 -TRANS-muman40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MAXILEN-200000000
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-NO MAAP -LARREQUERY -NGG SCORES=0 -MAIT -DSPBELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THERADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                        (without alignments)
695.153 Million cell updates/sec
                                                                                                        December 17, 2003, 14:50:33 ; Search time 1538.36 Seconds
                                                                                                                                                                                    233
1 EPLQARAHEMPAQKQPPADD.....IYFSGDDSCSLQVPGSTKGL 44
               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                            - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                        22781392 seqs, 12152238056 residues
                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                               0.5
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Fgapop 6.0 , Fgapext
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BUG16655 UI. H.-DEO-BX117347 BX117347 AG171073 GWB1671.8 BIO21560 CW3-MT034 BN830493 K.EST0104 BN850493 K.EST0104 BN855129 K.EST0103 BN856053 K.EST0139 BN85503 K.EST0139 BN85553 K.EST0139 BN85553 K.EST0139 BN85553 K.EST0139 BN85563 K.EST0139 BN85563 K.EST0139 BN85563 UI.E.EJU-BN72350 UI.E.EJU-BN72350 UI.E.EJU-BN72350 UI.E.EJU-BN723181 EST2393 BN5246 WI.EST0137 BN723181 EST23985 AA321182 EST23983 BF89343 QV3-MT012 BR89343 QV3-MT012 BR89343 QV3-MT012 BR89343 QV3-MT012 BR89343 QV3-MT012 BR89343 QV3-MT012 BR89343 QV3-MT012 BR893139 QV3-MT012 BR893139 QV3-MT012 BR893139 QV3-MT012 BR893138 QV3-MT012 BR893138 QV3-MT012

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C01361 HUMGS000834

BF893379 QV3-MT012 BI021220 CM0-MT035

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/lab host="mHn108"
/lone lib="Soares MhHMPU SI"
/clone lib-"Soares MhHMPU SI"
/clone lib-"Soares MhHMPU SI"
/cormalized libraries (melanocyte 2NbHM, pregnant uterus normalized libraries (melanocyte 2NbHM, pregnant uterus normalized libraries (melanocyte 2NbHM, pregnant uterus normalized as tracer in a subtractive hybridization, this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223,
340488-34479, and 444488-489479.
2 others
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Home sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 422)
Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,
Radelof, U., Schneider, D. and Korn, B.
Human Unigenseet - RZPD3
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seg primer:
M13r, Primer seguence: TTTCACACAGGAACAGCTATGAC.
                                                                                                                                                                Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
RZPD Dieutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGP98H134549.
RZPD; IMAGP98H134549.
RZPDILB; I.M.A.G.E. CDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB NO.972)
http://www.rzpd.de/cloneCardeb/Cgi-
bin/showLib.pl.cgi/response71ibNo-972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
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/organism="Homo sapiens"
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//dow_stage="Adult"
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//note="Grgan: marrow; Vector: puc18; Site_1: Smal; Site_2:
Smal; A mini-library was made by cloning products derived
from ORESTES POR (U.S. Letters Patent application No. 196
//16 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.22 DAX099382 Soares NHHMPu_S1 Homo sapiens cDNA clone IMAGp998H134549; IMAGE:1858620, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                Tel: +55-11-2704922
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CMO&t2=CMO-MT0351-150101-736-b03&t3=2001-01-15&t4=1)
Seg primer: puc 18 forward
High quality sequence store: 21
High quality sequence store: 307.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H. Erustein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                  Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProleuGlnAlaArgAlaHisGluMetProAlaGlnLysGlnProProAlaAspAspGln
                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                               Unpublished
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// db xref="taxon:9606"
// clone="IMARA"
// tissue type="Peoled human melanocyte, fetal heart, and pregnant uterus"
// lab host="markna"
// lone lib="Soares NhHMPu Sl"
// lone lib="Soares NhHMPu Sl"
// lone lib="Goares NhHMPu Sl"
// lone lib="organ: mixed (see below); vector: pr7T3D-Pac
// (Pharmacia) with a modified polylinker; Site l: Not I;
// Site_2: Bco RT; Equal amounts of plasmid DNA_Irom three
normalized libraries (melanocyte 2NbHW, pregnant uterus
// NhHDV, and fetal heart NbHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
// consisted of I.M.A.G.E. clones 260232-265223,
// a40488-3449949, and 444488-489479."
// lab tracer in a lone in a lone in the labers
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  ox74a06.x1 Soares NhHMPu S1 Homo sapiens cDNA clone IMAGE:1662034 3' similar to gb:X65977 NEUTROPHIL DEFENSIN 4 PRECURSOR (HUMAN);,
                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
I (bases 1 to 458)
NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                          National cauce.

Tumor Gene Index.

Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 637 Std Error: 0.00
Seq primer: -40ml3 fwd. BT from Amersham
High quality sequence stop: 446.
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/organism="Homo sapiens"
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                                       mRNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases 1 to 5)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,Y., Wylie,Y., Wylie,T., Waterston,R., Steptoe,M., Tan,F., Theising,B.,
WashU-NCI human EST Project
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                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 484.
Location/Qualifiers
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                                                                                                                                                                                                                                                                          Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
mol_type="mRNA"
db_xref="GDB:1316190"
db_xref="taxon:9606"
/clone="thAGB:409405"
/eex="unknown"
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PRECURSOR (HUMAN);, mRNA sequence.
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                 AA722853.
AA722853.1 GI:2740560
                                                                     Homo sapiens (human)
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                                                            311 AGGGGCATG 303
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1 (bases 1 to 542)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Location/Qualifiers
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 633 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                           AspValValIleTyrPheSerGlyAspAspSerCysSerLeuGlnValProGlySerThr 41
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                                                                                                  LysGlyLeu 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /Clone lib="Soares NhHMPu S1"
//Clone lib="Soares NhHMPu S1"
//note="Ozgan: mixed (see below); Vector: pT7T3D-Pac
//note="Ozgan: mixed (see below); Vector: pT7T3D-Pac
//pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G. Clones 260232-265223,
340488-345479, and 484488-489479."
51 a 134 c 136 g 119 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Pooled human melanocyte, pregnant uterus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="IMAGE:1858620"
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69.77%
53.49%
48.93%
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Matches:
Conservative:
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VERSION
KEYWORDS
                                                                                                                                                                                                     US-10-045-180A-5 (1-44) x BU616655 (1-634)
                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
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DEFINITION
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No.:
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  389 GACATATCTATTTCCTTTGCATGGGATAAAAGCTCTGCTCTTCAGGTTTCAGGCTCAACA
                                                                                              449 CCACTCCAGGCAAGAGGTGATGAGGCTCCAGGCCAGGAGCCAGGAGCCAGGAGACCAG 390
                                                    22
                                                                                                                                                     N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BU616655 634 bp mRNA linear EST 23-SEP-2002 UI-H-DF0-ben-n-14-0-UI.sl NCI CGAP DF0 Homo sapiens cDNA clone UI-H-DF0-ben-n-14-0-UI 3', mRNA sequence.
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National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq_primer: M13 FORWARD
                                       AspValVallleTyrPheSerGlyAspAspSerCysSerLeuGlnValProGlySerThr 41
                                                                                                                                                ProLeuGlnAlaArgAlaHisGluMetProAlaGlnLysGlnProProAlaAspAspGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 634)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /Clone lib="NCI CGAP DF0"

//Clone lib="NCI CGAP DF0"

//note="Oggan: Bone; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP DF0 is a cDNA library containing the following tissue(s): Subchondral Bone. The library was constructed according to Bonaldo, Lemnon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence tag for this library is TAG_LIB=UI-H-DF0
TAG_TISSUE=subchondral bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="UI-H-DF0-ben-n-14-0-UI"
/tissue_type="Subchondral Bone"
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/db_xref="taxon:9606"
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Matches:
Conservative:
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Minimum :
Maximum !
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-Q=/cgn2_1/USPTO_spool_p/US10045180/runat_17122003_145023_12520/app_query.fasta_1.860
-Q=/cgn2_1/USPTO_spool_p/US10045180/runat_17122003_145023_12520/app_query.fasta_1.860
-DB=N_Geneseq_19Jun03 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCI=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=buman40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE-LOCAL -OUTFMT=pto -NORM=ext -HARPSIZES=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10045180_GGGN_1 1_835_@runat 17122003_145023_12520 -NCPU=6 -ICPU=3
-NO_MMAD -LARGEQUERY -NEG_SCORES=0 -WALT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Run on
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           score
                                                    Pred. No.
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DB seq length: 2000000000
               greater
                                                                                                 N Geneseq 19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*

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18: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*

19: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*

20: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*

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22: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*

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27: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*

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           is the number of results predicted by chance ater than or equal to the score of the result
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Ygapop 10.0,
Fgapop 6.0,
Delop 6.0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2552756 seqs, 1349719017 residues
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Copyright (c) 1993 - 2003 Compugen Ltd.
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and is derived by analysis of the total score distribution.

# SUMMARIES

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AAX26697 ID AAX21 XX AC AAX21 XX AC AAX21 XX DT 18-UT XX DE CDNA XX XX Humaa XX KW Cytol KW endow KW endow KW endow KW AIDS XX XX XX XX XX XX XX XX XX	42 43 45	16666666666666666666666666666666666666	8 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	NO. 122
26697; 26697; 7UN-19; TUN-19; an defi ostatie ostatie s; immm		73.54 73.54 72.5 72.7 72.7	101 90 90 83 83 82 80 80 80 80 78.5 78.5 78.5 78.5 78.5 78.5	Score 233 233 209 114 104 101
anda (f)				Query Match 100.0 100.0 89.7 48.9 44.6 43.3
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BP.  defensin (Def-X) pricrobial; antiparasi ammation; tissue repostatic regulation; riasis; ss.	AAT30735 AAD47375 ABK39009 ACA11338 ALIGNMENTS	AAC53218 AAC53218 AAT30737 ABC36740 ABC60009 ABC60009 ABC11202 AAT30738 AAT30738 AAT30738	ACA56600 ABN59997 AAC66925 AAC66925 AAC66925 AAC66924 AAD51768 AAQ53216 ABQ60783 AAH57427 ABC66927 ABC66927 AAC66927 AAC66927 AAC66927 AAC66927 AAC66927 AAC66927 AAC66927 AAC9468 AA	ID  AAX26697  AAX26698  AAX26696  AAX63473  AAD51767  AAH57220  AA053271
otein. tic; pesticide; air; cancer; melanoma;	Rat cryptdin 3 cDN Human LP321 DNA. cDNA encoding lung Human lung adenoca	sus macaque omic sequenc cryptdin 2 cryptdin 2 an GENSET co an colon car an colon car an polynucle cryptdin 3 cryptdin 3	gnallir man coc eta def acaque ulatta encodi fensin testine lon car acaque encesin fensin fensin fensin fensin fensin fensin fensin fensin fensin fensin fensin fensin fensin	Description  CDNA sequence enco CDNA sequence enco Nucleotide sequenc Human CDNA #473 di Human retrocyclin Human intestine sp

### cDNA sequence encoding human defensin (Def-X) protein. 18-JUN-1999 AAX26697; AAX26697 standard; cDNA; 453 BP AIDS; immune deficiency; psoriasis; ss. (first entry)

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RESULT 2
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ID AAX2
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AC AAX2
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Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence encodes human defensin (Def-X). The Def-X CC polypeptide can be used as an antimicrobial, antiparasitic agent or CC a pesticide. The Def-X polypeptide can be used as a cytostatic (especially anticancer) agent, and as an agent for modulating processes CC of inflammation, tissue repair and endorine (especially corticostatic) regulation. The polypeptide can be used in a composition for external topical use, especially in a cosmetic composition. Compositions (containing Def-X can be used for prevention and treatment of microbial and parasitic infections, especially where the microbial or parasitic infections or especially where the microbial or parasitic infections are gram-positive or -negative bacterial infections or mycobacterial, fungal or spirochaete infections, or where the viral infections are associated with enveloped viruses, especially HIV. The compositions can used for prevention and/or treatment of cancers, compositions can used for prevention and/or treatment of cancers capacially in the case of AIDS, or preventing immunity, the capacially in the case of AIDS, or preventing immunity inflammatory processes, especially in the case of AIDS, or preventing as well as for modulating inflammatory processes, especially in the case of AIDS or preventing the case of chronic inflammatory calsories.
   cDNA sequence encoding human defensin
                                   18-JUN-1999
                                                                  AAX26698
                                                                                              AAX26698 standard; cDNA; 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human defensin polypeptide Def-X - useful as antimicrobial agent, anticancer agent, pesticide, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
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                                                                                                                                                                                                                                                                              GluProLeuGlnAlaArgAlaHisGluMetProAlaGlnLysGlnProProAlaAspAsp 20
                                                                                                                                                                                                                                     GlnAspValVall1eTyrPheSerGlyAspAspSerCysSerLeuGlnValProGlySer 40
                                                                                                                                                                                      ThrLysGlyLeu 44
                                                                                                                                                                                                                CAGGATGTGGTCATTTACTTTTCAGGAGATGACAGCTGCTCTTCTTCAGGTTCCAGGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENSET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВÞ;
                                  (first entry)
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(Def-X) protein.
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Percent Similarity:
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence encodes human defensin (Def-X). The Def-X
C polypeptide can be used as an animicrobial, antiparasitic agent or
CC a pesticide. The Def-X polypeptide can be used as a cytostatic
CC (especially anticancer) agent, and as an agent for modulating processes
CC of inflammation, tissue repair and endocrine (especially corticostatic)
CC regulation. The polypeptide can be used in a composition for external
CC containing pef-X can be used for prevention and treatment of microbial
CC and parasitic infections, especially where the microbial or parasitic
CC infections are Gram-positive or -negative bacterial infections or
CC infections are associated with enveloped viruses, especially HSV and HIV.
CC especially melanomas, or liver cancer, prostate cancer, non-small-cell
CC lung cancer or colorectal carcinoma, and for enhancing immunity,
CC especially in the case of AIDS, or prevention deficiency,
CC inflammatory processes, especially in the case of formations as well as for modulating
CC inflammatory processes, especially in the case of AIDS, or preventions as well as for modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 453 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human defensin polypeptide Def-X - useful as antimicrobial agent, anticancer agent, pesticide, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5;
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                                                                                                                                                                                     1 GluProLeuGlnAlaArgAlaHisGluMetProAlaGlnLysGlnProProAlaAspAsp
ThrLysGlyLeu 44
                                                               CAGGATGTGGTCATTTACTTTTCAGGAGATGACAGCTC
                                                                                                         GlnAspValVallleTyrPheSerGlyAspAspSerCysSerLeuGlnValProGlySer 40
                                                                                                                                                              GAGCCGCTCCAGGCAAGAGCTCATGAGATGCCAGCCCAGAAGCAGCCTCCAGCAGATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fig 4; 56pp;
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RESULT 3
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                                                                                                                                                                                                                                                                                                                      (especially anticance) agent, and as an agent for modulating processes of inflammation, tissue repair and endocrine (especially corticostatic) of inflammation, tissue repair and endocrine (especially corticostatic) or regulation. The polypeptide can be used in a composition for external control use, especially in a cosmetic composition. Compositions or control of microbial or control of infections or control of microbial or parasitic infections, especially where the microbial or parasitic infections or endocrine infections or mycobacterial, fungal or spirochaete infections, or where the viral confections are associated with enveloped viruses, especially HSV and HIV. The compositions can used for prevention and/or treatment of cancers, cespecially melanomas, or liver cancer, prostate cancer, non-small-cell lung cancer or colorectal carcinoma, and for enhancing immunity, cespecially in the case of AlDS, or preventing immune deficiency, cespecially in the treatment of psoriasis, as well as for modulating inflammatory processes, especially in the case of chronic inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence encodes human defensin (Def-X). The Def-X polypeptide can be used as an antimicrobial, antiparasitic agent or a pesticide. The Def-X polypeptide can be used as a cytostatic (especially anticancer) agent, and as an agent for modulating processes
                                                                                                                                                                                                                                                                                     Sequence 4415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human defensin; Def-X; antimicrobial; antiparasitic; pesticide; cytostatic; anticancer; inflammation; tissue repair; endocrine regulation; corticostatic regulation; cancer; melanom
                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Fig 2; 56pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        anticancer agent,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human defensin polypeptide Def-X - useful as antimicrobial agent,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GEST )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleotide sequence of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JUN-1999
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                            21
                                                                     GluProLeuGlnAlaArgAlaHisGluMetProAlaGlnLysGlnProProAlaAspAsp
                  GlnAspValValIleTyrPheSerGlyAspAspSerCysSerLeuGlnValProGly 39
                                                           GAGCCGCTCCAGGCAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 deficiency; psoriasis; ss.
                                                                                                                                                                                                                                                                                   B₽;
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                                                                                                                                                                                                                                                                                 14 other;
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RESULT 4
ABX63473
ID ABX6
                                                                                                                         This invention relates to a combination comprising several cDNAs that C are differentially expressed in activated vascular tissue. The invention CC also discloses a high throughput method for detecting differentially CC expressed cDNAs in a sample. The cDNAs of the invention may have CC antiarteriosclerotic; cytostatic; cardiant; hypotensive; antidiabetic; CY gynaecological; vasotropic and cerebroprotective activities and may be used in gene therapy. The cDNAs of the invention may be used in a compound that specifically binds a cDNA of the convertion of the compounds to identify a molecule or compound that specifically binds a cDNA of the compounds to identify a molecules or compound that specifically binds a cDNA of the compounds to identify a ligand that specifically binds to the protein, or to produce or purify an antibody to the protein that can compound to detect a protein in a sample or purify a natural or compounds to identify a ligand that specifically binds to the protein from a sample. The nucleotides may be useful for creambinant protein from a sample. The nucleotides may be useful for creambinant protein from a sample. The nucleotides may be useful for creampounds in a treating, or monitoring the progression of creatment of a vascular disease, e.g. atherosclerosis, cancer, coronary creatment of a vascular disease, e.g. atherosclerosis, cancer, coronary creatment of a vascular disease, e.g. atherosclerosis, cancer, coronary creatment of a vascular disease, e.g. atherosclerosis, cancer, coronary creatment of avascular disease, e.g. atherosclerosis, cancer, coronary creatment of avascular protein and the proteins encoded by the coronary creatment of a coronary research proteins and coronary creatment of avascular tises to the proteins encoded by the coronary creatment of dispnosing pre-pathologic disorders, and chronic coronary creatment of the protein that is differentially expressed in activated vascular tissue.
                                     represents a cDNA of the invention that is differentially expressed in activated vascular tissue.

Note: The sequence data for this patent did not form part of the specification, but was obtained in electronic format directly from USPTO at http.seqdata.uspto.gov/sequence.html?DocID=20020137081.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Combination for diagnosing, staging, treating, or monitoring the progression of treatment of a vascular disease, e.g. atherosclerosis, comprises several CDNAs that are differentially expressed in activated vascular tissue -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page -; 18pp; English.
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08-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cDNA #473 differentially expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABX63473;
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2001US-260483P.
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Sequence 860 BP;

216 A;

211 C;

192 G; 241 T;

other

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AC AADS
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV; human immunodeficiency virus; bacterial vaginosis; ophthalmic infection; antibiotic modelling; antimicrobial; human; gene; ds.
                     P-PSDB; AAE33811, AAE33860
                                                                                 Lehrer RI, Waring AJ,
                                                                                                                                                                            18-APR-2001;
                                                                                                                                                                                                                      18-APR-2002;
                                                                                                                                                                                                                                                                                                               WO200285401-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sig_peptide
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                                          2003-103387/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CACTCCAGGCAAGAGGTGATGAGGCTCCAGGCCAGGAGCAGCGTGGGCCAGAAGACCCAG
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                                                                                                                                CALIFORNIA
                                                                                                                                                                            2001US-284855P
                                                                                                                                                                                                                         2002WO-US12353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /partial 63..126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "Human retrocyclin precursor protein" /transl_except= (pos:124..126, aa:Xaa) /transl_except= (pos:304..306, aa:Xaa) /transl_except= (pos:361..363, aa:Xaa) /transl_except= (pos:409..411, aa:Xaa) /note= "Xaa corresponds to in-frame stop codon; No start and stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= l
127..495
                                                                                                                                                                                                                                                                                                                                                                                                   /product= "Mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                           product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                *tag= c
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69.77%
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                                                                                 Hong
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Gaps:
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                                                                                    TB;
                                                                                                                                                                                                                                                                                                                                                       retrocyclin
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RESULT 6
AAH57220
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroviral infection cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiency virus) sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin-mediated killing is useful for modelling and screening novel antibiotics. The invention is also useful in general
                                                                                                                                                                                                                                                  Human; tissue specific; diagnosis; brain; heart; skeletal muscle; lung; liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss; metabolic disease; developmental disease; cytostatic; immunomodulatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections of treating patients having the infections, such as HIV, sexually transmitted diseases, vaginosis
                                                                                                            04-NOV-1999;
                                                                                                                                    02-NOV-2000; 2000WO-US30396
                                                                                                                                                                                                                                                                                                     Human intestine specific cDNA sequence SEQ ID NO:60
                                                                                                                                                                                                                                                                                                                                                           AAH57220;
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                                  WPI; 2001-291057/30
                                                                                                                                                                  10-MAY-2001
                                                                                                                                                                                        WO200132927-A2
                                                                                                                                                                                                                  Homo варіелв.
                                                                                                                                                                                                                                           neuroprotective;
                                                                                                                                                                                                                                                                                                                                 10-SEP-2001
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                                                                                    (INCY-) INCYTE GENOMICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                      256 GCGAGAGGCTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is human retrocyclin DNA.
                                                          Seilhamer
                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                            99US-0163508
                                                                                                                                                                                                                                         gene therapy; cancer; immunopathology; neuropathology
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104.00
68.18%
50.00%
44.64%
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                                                         'n,
                                                                                                                                                                                                                                                                                                                                                                                    294
                                                          Watson
                                                                                                                                                                                                                                                                                                                                                                                   BP
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infections
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New cell and tissue specific polynucleotides useful for diagnosis, prognosis or monitoring of treatments for disorders where the gene

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mimetics, peptides, proteins, agonists, antagonists, antibodies or their fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical agents. Expression of (1) in a sample indicates the differentiation of embryonic stem cells into a tissue selected from brain, heart, kidney, liver, lung, skeletal muscle or pancreatic tissues. (1) and (11) are used to produce an expression profile that defines a metabolic or developmental process, treatment, condition, disease or disorder. The gene profile can be used for diagnosis, prognosis or monitoring of treatments and for investigating a predisposition to a disorder where the gene is associated with a
            18-MAY-1993;
                                        09-DEC-1993.
                                                                    WO9324513-A1
                                                                                                                                                                                                 Gastrointestinal defensin peptide; GID; pharmaceutical; Paneth cell; antimicrobial; anti-inflammatory; diagnosis;
                                                                                                                                                          Homo sapiens
                                                                                                                                                                                         contact
                                                                                                                                                                                                                                                 Sequence encoding gastrointestinal defensin human defensin 6.
                                                                                                                                                                                                                                                                                              25-MAR-2003
17-JUN-1994
                                                                                                                                                                                                                                                                                                                                          AAQ53217;
                                                                                                                                                                                                                                                                                                                                                                     AAQ53217 standard; cDNA; 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequences (I). (I) can have cytostatic, immunomodulatory and neuroprotective activities, and can be used in gene therapy. (I) and proteins (II) encoded by then are used in high throughput screening assays to select DNA molecules, RNA molecules, peptide nucleic acids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH57161 to AAH57576 represent cell and tissue specific polynucleotide sequences (I). (I) can have cytostatic, immunomodulatory and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93
                                                                                                                                                                                        disinfectant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunopathology or neuropathology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ThrLys 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlnAspValValIleTyrPheSerGlyAspAspSerCysSerLeuGlnValProGlySer 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ### CATCCACTGCAGGCAAAAGCTTATGAGGCTGATGCCCAGGAGCAGCGTGGGGCAAATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluProLeuGlnAlaArgAlaHisGluMetProAlaGlnLysGlnProProAlaAspAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                 ACAAGG 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGGACTTTGCCGTCTCCTTTGCAGAGGATGCAAGCTCAAGTCTTAGAGCTTTGGGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              294 BP; 72 A; 80 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 95; 327pp; English.
                                                                                                                                                                                                                                                                                          (updated)
(first entry)
          93WO-US04740.
                                                                                                               Location/Qualifiers
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71.43%
50.00%
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                                                                                                                                                                                                                                                                                                                                                                      BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
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12
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RESULT 8
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCOre:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  defensin peptides. Prof. the libraries were human genomic and CDNA
libraries. Hybridisation and partial sequence analysis of the
identified clones contained previously characterised myeloid derived
defensin sequences as well as new defensin related sequences. Two
clones expressing new defensin related sequences were extensively
characterised and found to contain genes selectively expressed in
paneth cells of the small intestin. These paneth cell-derived
defensins are designated human defensin 5 and human defensin 6 and
are referred to as gastrointestinal defensin beddensin 6 and
the deduced AA sequences of the defensin 5 cDNA with the
previously reported preprodefensian sonws significant similarity.
The deduced AA sequence of defensin 6 cDNA bas features similar to
defensin 5 and the previously reported preprodefensins.

(Updated on 25-MAR-2003 to correct PN field.)
                                                   Human; probe; ss; array element; Parkinson's disease; signalling pathway population; cancer; adenocarcinoma; leukaemia; immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
                           Homo sapiens
                                                                                                                                                     06-JUN-2003
                                                                                                                    Human signalling pathway polynucleotide probe SEQ ID NO 1198
                                                                                                                                                                                    ACA56600
                                                                                                                                                                                                                 ACA56600 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A probe (D5' oligo) having the sequence given in AAQ53219 (claimed) was used to screen a population of clones to identify novel defensi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; page 48-49; 97pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gastrointestinal defensin peptide(s) and anti-inflammatory agents and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1993-405719/50
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                                                                                                                                                                                                                                                                                                            41
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                                                                                                                                                                                                                                                                                                                                      CAGGACTTTGCCGTCTCCTTTGCAGAGGATGCAAGCTCAAGTCTTAGAGCTTTGGGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                    GATCCACTGCAGGCAAAAGCTTATGAGGCTGATGCCCAGGAGCAGCGTGGGGCTAATGAC 156
                                                                                                                                                                                                                                                                                                                                                                                                                    GluProLeuGlnAlaArgAlaHisGluMetProAlaGlnLysGlnProProAlaAspAsp
                                                                                                                                                                                                                                                                               ACAAGG 222
                                                                                                                                                                                                                                                                                                          ThrLys 42
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    useful as antimicrobial detecting gastrointestinal

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RESULT 9
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a combination which, comprises a number of comply nucleotide probes comprising a sequence selected from one of the 1490 companies of the probes comprising a sequence selected from one of the 1490 companies of the probes comprising a sequence selected from one of the 1490 companies of the microarray for monitoring the expression of a number companies of the microarray is useful in the diagnostic substituted and treatment regimens, drug companies of the microarray is and treatment regimens, drug discovery and development, toxicological and carcinogenicity studies, companies of the paranacogenomics. The microarray is also useful for monitoring progression of diseases and for developing sophisticated compination is also useful for purifying a subpopulation of mRNAs, cDNAs and genomic fragments and in research and diagnostic applications. The combination is also useful for purifying a subpopulation of mRNAs, cDNAs and genomic fragments and in research and diagnostic applications. The companies of the signaling pathway populations which can be used to diagnose constitutions diseases including cancer e.g. adenocarcinoma and leukaemia, constitutions of the invention of the invention of the present sequence represents a polynucleotide corobe of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probe
Note:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
 28-JUN-2002
                                   ABN59997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 452 BP; 124 A; 118 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not form part specification but was obtained in electronic format direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 1198; 65pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polynucleotides
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                                                                   ABN59997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seqdata.uspto.gov/sequence.html?DocID=06500938B1.
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                                                                                                                                                                                                                                 GlnAspValValIleTyrPheSerGlyAspAspSerCysSerLeuGlnValProGlySer
                                                                                                                                                                                                                                                                     GATCCACTGCAGGCAAAAGCTTATGAGGCTGATGCCCAGGAGCAGCGTGGGGCAAATGAC
                                                                                                                                                                                                                                                                                                     GluProLeuGlnAlaArgAlaHisGluMetProAlaGlnLysGlnProProAlaAspAsp
                                                                   standard;
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                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESTS). They can be used to stimulate cell growth, to regulate haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. parkinson's disease. The present sequence is a coding sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; antianaemic; vulnerary; antiinflammatory; immunomodulator; antiinfertility; cerebroprotective; cytostatic; rheumatic; gene temporotective; antiparkinsonian; protein therapy; EST;
               Human theta defensin coding sequence SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 An isolated polynucleotide for treating diseases associated encoded polypeptide such as cancer and multiple sclerosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang YT, Liu C,
Xue AJ, Yang Y,
                                           27-MAR-2001
                                                                                              AAC66930
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DB; ABB97584.
                                                                                                                                                168
                                                                                                                                                                                                   108 GATCCACTGCAGGCAAAAGCTTATGAGGCTGATGCCCAGGAGCAGCGTGGGGCAAATGAC
                                                                                                                                                                     21 GlnAspValVallleTyrPheSerGlyAspAspSerCysSerLeuGlnValProGly
                                                                                                                                                                                                                          1 GluProLeuGlnAlaArgAlaHisGluMetProAlaGlnLysGlnProProAlaAspAsp
                                                                                            standard;
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                                          (first entry)
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Wehrman
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RESULT 11
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  10-MAY-2000; 2000WO-US12842
                                                                              WO200068265-A1
                                                                                                                      Rhesus macaque.
                                                                                                                                                                                    Theta
                                                                                                                                                                                                                        Rhesus macaque theta defensin RTD-1b coding sequence.
                                                                                                                                                                                                                                                                27-MAR-2001
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                                          16-NOV-2000.
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                                                                                                                                                          defensin; a
; helminth;
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                                                                                                                                                            antimicrobial;
disinfectant;
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; disinfectant;
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                                                                                                                                                        cyclic; bacterium;
food preservative;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides theta defensin peptides and analogues which have antimicrobial activity. They can be used in the treatment bacterial, viral, fungal, protozoan and helminthic infections, in disinfectants and as food preservatives.
                                                                                                                                                                                                                                                                          Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV; human immunodeficiency virus; bacterial vaginosis; ophthalmic infection; antibiotic modelling; antimicrobial; rhesus monkey; theta defensin 1b;
                                                                                                                                                                                                                                                                                                                                                       Macaca mulatta RTD2 DNA.
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WO200285401-A1
                                                                   mat_peptide
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                                                                                                                                                                                                                                                        RTD2; gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiency virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin-mediated killing is useful for modelling and screening novel antibiotics. The invention is also useful in gene therapy. The present sequence is rhesus monkey theta defensin 1b precursor, RTD2 DNA. This sequence is used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections of treating patients having the infections, such as HIV, sexually transmitted diseases, vaginosis
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                                                                                                                                                                               Theta defensin;
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                                                                                                                                               cyclic; bacterium;
food preservative;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV, human immunodeficiency virus; bacterial vaginosis; ophthalmic infection; antibiotic modelling; antimicrobial; rhesus monkey; theta defensin 1A;
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                                                                                                                                                                                                                                                                                                                                                             Socation/Qualifiers
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/product=

"Mature RTD3 protein"

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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroviral infection in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiency virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin-mediated killing is useful for modelling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually transmitted diseases, vaginosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and screening novel antibiotics. The invention is also useful in gene therapy. The present sequence is rhesus monkey theta defensin 1A precursor, RTD3 DNA. This sequence is used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-103387/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200285401-A1
            Gastrointestinal defensin peptide; GID; cell; antimicrobial; anti-inflammatory; contact disinfectant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 52; 72pp; English.
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                                                                  Sequence encoding gastrointestinal defensin (GID) peptide called human defensin 5.
                                                                                                           25-MAR-2003
17-JUN-1994
                                                                                                                                                   AAQ53216;
                                                                                                                                                                             AAQ53216 standard; cDNA; 424 BP
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diagnosis;
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                                                                                                                                US-10-045-180A-5 (1-44) x AAQ53216 (1-424)
                                                                                                                                                                                                                                                   Pred. No.:
                                                                                                                                                                                                                                                                                                                             A probe (D5' oligo) having the sequence given in AAQ53219 (claimed)
was used to screen a population of clones to identify novel defensin
clother defensin peptides. Pref. the libraries were human genomic and cDNA
clibraries. Hybridisation and partial sequence analysis of the
clibraries. Hybridisation and partial sequence analysis of the
clidentified clones contained previously characterised myeloid derived
defensin sequences as well as new defensin related sequences. Two
clones expressing new defensin related sequences were extensively
characterised and found to contain genes selectively expressed in
claracterised and found to contain genes selectively expressed in
claracterised and found to defensin. These Paneth cell-derived
defensins are designated human defensin 5 and human defensin 6 and
claracteristic to as gastrointestinal defensin peptides. Comparison
of the deduced AA sequences of the defensin 5 cDNA with the
previously reported preprodefensins shows significant similarity.

The deduced AA sequence of defensin 6 cDNA bas features similarity
clided to a specific of the defensin 5 cDNA with the
previously reported preprodefensins.

Clided the previously reported preprodefensins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gastrointestinal defensin peptide(s)
and anti-inflammatory agents and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1993-405719/50.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-MAY-1992;
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                    GlnAspValValIleTyrPheSerGlyAspAspSerCysSerLeuGlnValProGlySer
 CAGGACCTTGCTATCTCCTTTGCAGGAAATGGACTCTCTGCTCTTAGAACCTCAGGTTCT
                                                                   GAGTCACTCCAGGAAAGAGCTGATGAGGCTACAACCCAGAAGCAGTCTGGGGAAGACAAC
                                                                                            GluProLeuGlnAlaArgAlaHisGluMetProAlaGlnLysGlnProProAlaAspAsp
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    useful as antimicrobial detecting gastrointestinal

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Search completed: December Job time : 166 Becs

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Result
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Maximum DB seq length: 200000000
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Listing first 45 summaries
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Perfect score:
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-Q=/cgn2 1/USFTO_spool_p/US10045180/runat_17122003_145026_12635/app_query.fasta_1.860
-Q=/cgn2 1/USFTO_spool_p/US10045180/runat_17122003_145026_12635/app_query.fasta_1.860
-DB=PublIshed_Applications_NA -QFMT=fastap -SUPFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITGS=bite -STRAT=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=20000000000 -USER=US10045180_GCNN_1 1_174_@runat_17122003_145026_12635
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT_-DSPBLOCK=100
-LONGLOG -DEV_TIMEDUT=120 -WARN_TIMEDUT=30 -THREADS=1 -XGAPDP=10 -XGAPEXT=0.5
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                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
          Score
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| Cgn2_6/ptcdata/2/pubpna/PCT_NEW_PUB.seq:*
| Cgn2_6/ptcdata/2/pubpna/USO6_PUBCOMB.seq:*
| Cgn2_6/ptcdata/2/pubpna/USO6_PUBCOMB.seq:*
| Cgn2_6/ptcdata/2/pubpna/USO6_PUBCOMB.seq:*
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ORGANISM. Homo sapiens SEQUENCE DESCRIPTION: SEQ ID NO: US-10-013-770-2
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Alignment Scores:
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Publication No. US20020182703A1
GENERAL INFORMATION:
APPLICANT: Bougueleret, Lydie
APPLICANT: Chumakov, Ilya
                                                                                                                                                                                                        SEQ ID NO 2
                                                                                                                                                                                                                                                            TITLE OF INVENTION: Human Defensin Polypeptide Def-X, Genomic DNA and cDNA, Compositi TITLE OF INVENTION: Containing Them and Applications to Diagnosis and to Therapeutic CURRENT APPLICATION NUMBER: US/10/045,180A
CURRENT FILING DATE: 2001-10-18
PRIOR APPLICATION NUMBER: US 9/486,580
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: PCT/FR98/01864
PRIOR APPLICATION NUMBER: PCT/FR98/01864
PRIOR APPLICATION NUMBER: PCT/FR98/01864
PRIOR APPLICATION NUMBER: FR 97/10823
PRIOR FILING DATE: 1998-08-29
PRIOR FILING DATE: 1997-08-29
                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
                                                      FEATURE:
NAME/KEY: CDS
LOCATION: (52)..(336)
OTHER INFORMATION: Def-X coding sequence
                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATIÓN NUMBER: 40,637
REFERENCE/DOCKET NUMBER: GENSET.064C1
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 453 BASE PAIRS
TYPE: NUCLEOTIDE
STRANDEDNESS: DOUBLE
                                                                                                                                                                                   ENGTH: 453
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/486,580
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Hart, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: LINEAR MOLECULE TYPE: cDNA ORIGINAL SOURCE:
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Publication No. US20020115151A1
GENERAL INFORMATION:
APPLICANT: GENSET SA
                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/10/013,770
PILING DATE: 10-Dec-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/486,580
FILING DATE: <UNKnown>
ATTORNEY/AGENT INFORMATION:
NAME: Hart, Daniel
REGISTRATION NUMBER: 40,637
REGISTRATION NUMBER: 40,637
                                                                        FEATURE:
                                                                                                                                                                                   FEATURE
                                                                                                                                                                                                                    TOPOLOGY: LINEAR MOLECULE TYPE: DNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: HUMAN DEFENSIN DEF-X GENE AND DIAGNOSTIC AND COMPOSITION CONTAINING SAME AND DIAGNOSTIC AND THERAPEUTIC APPLICATIONS
               FEATURE:
                                                                                                                              FEATURE:
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                                                                                                                                                                                                                                                                            TYPE: NUCLEOTIDE STRANDEDNESS: DOUBLE
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STATE: California
                                                    NAME/KEY:
                                                                                                            NAME/KEY:
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NAME/KEY:
                                   LOCATION:
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                                                                                                                                            LOCATION:
                                                                                                                                                                                                                                                                                                                   LENGTH: 4415 BASE PAIRS
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                                                    Exon 3
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CURRENT APPLICATION NUMBER: US/10/045,180A

CURRENT FILING DATE: 2001-10-18

PRIOR APPLICATION NUMBER: US 09/486,580

PRIOR FILING DATE: 2000-02-25

PRIOR APPLICATION NUMBER: PCT/FR98/01864

PRIOR FILING DATE: 1998-08-28

PRIOR FILING DATE: 1997-08-29

PRIOR APPLICATION NUMBER: FR 97/10823

PRIOR PILING DATE: 1997-08-29

NUMBER OF SEQ ID NOS: 12
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Human Defensin Polypeptide Def-X, Genomic DNA and cDNA, Composit
TITLE OF INVENTION: Containing Them and Applications to Diagnosis and to Therapeut:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bougueleret, Lyc
APPLICANT: Chumakov, Ilya
NAME/KEY: misc_feature
LOCATION: (970)..(970)
OTHER INFORMATION: n = a,
                                                                        NAME/KEY: misc feature
LOCATION: (670)..(670)
OTHER INFORMATION: n =
                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (1)...(4415)
OTHER INFORMATION: Def-X
                                                                                                                                                      LOCATION: (143) ... (143)
OTHER INFORMATION: n =
                                                                                                                                                                             NAME/KEY: misc feature LOCATION: (143)..(143)
                                                                                                                                                                                                                       OCATION: (85)..(85)
OTHER INFORMATION: n =
                                                                                                                                                                                                                                                       NAME/KEY: misc feature LOCATION: (85)..(85)
                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH: 4415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rence 1, Application US/10045180A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3523 CAGGATGTGGTCATTTACTTTTCAGGAGATGACAGCTGCTCTCTTCAGGTTCCAGGT 3579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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LOCATION:
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4276..4278
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Matches:
Conservative:
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NAME/KEY: misc_feature
LOCATION: (3406)..(3408)
OTHER INFORMATION: Translation initiation codon (ATG)
                                                                                              NAME/KEY: misc feature
LOCATION: (3394)..(3577)
OTHER INFORMATION: Exon
                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (3391)..(3393)
OTHER INFORMATION: splice acceptor site
                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (2367)..(2367)
OTHER INFORMATION: n = a
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NAME/KEY: misc_feature
LOCATION: (1974)..(1974)
OTHER INFORMATION: n = a,
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NAME/KEY: misc_feature
                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (2710)..(2780)
OCHER INFORMATION: L1 fragment insertion
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OTHER INFORMATION: n = a,
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OTHER INFORMATION: n = a,
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LOCATION: (1111)...(1111)
OTHER INFORMATION: n = a,
FEATURE:
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OTHER INFORMATION: n = a
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LOCATION: (2155)..(2335)
OTHER INFORMATION: Alu insertion
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OTHER INFORMATION: n = a,
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OTHER INFORMATION: n = a,
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LOCATION: (2117)..(211
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OTHER INFORMATION: Exon
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OTHER INFORMATION:
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OTHER INFORMATION: n = a,
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Sequence 8, Application US/10045180A

Publication No. US20020182703A1

GENERAL INFORMATION:

APPLICANT: Bugueleret, Lydie

APPLICANT: Chumakov, 11ya

ITITE OF INVENTION: Human Defensin Polypeptide Def-X, Gen

ITITE OF INVENTION: Containing Them and Applications to IPILE REFERENCE: GEN-100D1

CURRENT APPLICATION NUMBER: US/10/045,180A

CURRENT PILING DATE: 2001-10-18

PRIOR APPLICATION NUMBER: US 09/486,580

PRIOR APPLICATION NUMBER: PT/FR98/01864

PRIOR APPLICATION NUMBER: PT/FR98/01864

PRIOR FILING DATE: 1998-08-28

PRIOR APPLICATION NUMBER: FR 97/10823

PRIOR APPLICATION NUMBER: FR 97/10823

PRIOR APPLICATION NUMBER: FR 97/10823

PRIOR APPLICATION NUMBER: PT/FR98/01864

PRIOR APPLICATION NUMBER: FR 97/10823

PRIOR APPLICATION NUMBER: FR 97/10823
; NAME/KEY: CDS
; LOCATION: (52)..(345)
; COTHER INFORMATION: Def-4 (HNP-4) coding sequence
US-10-045-180A-8
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Query Match:
DB:
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                                                                                                                                                      SEQ ID NO 8
LENGTH: 542
                                                                                                                                                                                                                           PRIOR FILING DATE: 1997-08-29 NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: polyA signal LOCATION: (4374)..(4379) OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (4274)..(4276)
OTHER INFORMATION: Translation
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LOCATION: (4164)..(4379)
OTHER INFORMATION: Exon
                                                                                          FEATURE:
                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                   TYPE: DNA
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OTHER INFORMATION: splice acceptor site
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LOCATION: (4161)...(416
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LOCATION: (4123)..(4123)
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Percent Similarity:
Best Local Similarity:
Query Match:
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US-10-141-645-11
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Query Match:
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; OTHER INFORMATION: Incyte ID No.
US-10-044-090-473
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                               Sequence 11, Application US/10141645
Publication No. US20030144184A1
GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 473, Application US/10044090
Publication No. US20020137081A1
GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 860
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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Alan Waring
Alexander Cole
Teresa Hong
                                                                                                                                                                                         LysGlyLeu 44
                                                                                                                                                                                                                                    AspValValIleTyrPheSerGlyAspAspSerCysSerLeuGlnValProGlySerThr 41
                                                                                                                                                                                                                                                                                                         ProLeuGlnAlaArgAlaHisGluMetProAlaGlnLysGlnProProAlaAspAspGln
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RESULT 8
US-10-125-237-78
US-10-125-237-78
; Sequence 78, Application US/10125237
; Publication No. US20030022329A1
                                                                 APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20030022329A1el Nucleic Aci
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 791CIP2ADIV
CURRENT APPLICATION NUMBER: US/10/125,237
CURRENT FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 09/668,317
PRIOR APPLICATION NUMBER: 09/668,317
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-09-22
PRIOR PRILING DATE: 2000-04-18
PRIOR PRIOR APPLICATION NUMBER: 09/552,929
PRIOR FILING DATE: 2000-04-18
PRIOR FILING DATE: 2000-04-18
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Best Local Similarity:
Query Match:
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          SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 78
LENGIH: 1348
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APPLICANT:
APPLICANT:
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SEQ ID NO 11
LENGTH: 496
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APPLICANT:
APPLICANT:
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APPLICANT: Liu, Chenghua
APPLICANT: Zhou, Ping
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CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 60/284,855
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: Unassigned
PRIOR FILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
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TYPE: DNA
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NAME/KEY: CDS
LOCATION: (124)...(304)
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Wehrman, Tom
Wang, Jian-Rui
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Zhao, Qing A.
Xue, Aidong J.
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Asundi, Vinod
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICANT: Drmanac, Radoje T.

ITITLE OF INVENTION: No. US20030073099Alel Nucleic Acids and TITLE OF INVENTION: Polypeptides

FILE REFERENCE: 791CIP2A

CURRENT APPLICATION NUMBER: US/10/105,891

CURRENT FILING DATE: 2002-03-25

PRIOR APPLICATION NUMBER: 09/668,317

PRIOR FILING DATE: 2000-09-22

PRIOR PILING DATE: 2000-09-22

PRIOR PPLICATION NUMBER: 09/552,929

PRIOR PPLICATION NUMBER: 09/552,929

PRIOR PILING DATE: 2000-04-18

NUMBER OF SEQ ID NOS: 91

SOFTWARE: pt_FL_genes Version 2.0

SEQ ID NO 78
                                                Percent Similarity:
Best Local Similarity:
Query Match:
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US-10-045-180A-5 (1-44) x US-10-105-891-78 (1-1348)
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Best Local Similarity:
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Publication No. US20030073099A1
GENERAL INFORMATION:
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APPLICANT: Liu, (
APPLICANT: Zhou,
APPLICANT: Asundi
APPLICANT: Ren, I
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1143)
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APPLICANT:
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Wang, Jian-Rui
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Xue, Aidong J.
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Zhao, Qing A.
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Asundi, Vinod
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
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RESULT 11
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US-10-027-632-30053
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LENGTH: 592
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(592)
OTHER INFORMATION: n =
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ORGANISM: Human
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                                 ACA 337
                                                                       Thr 41
                                                                                                         CAGGAAATGGCTCATGCCTTTACATGGCATGAAAGTGCCGCTCTTCCGCTTTCAGGTGAG 334
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
                                                              Sequence 30053, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
ITTLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827,129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
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SEQ ID NO 30054
LENGTH: 592
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PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
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CURRENT FILING DATE: 2002-04-30
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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OTHER INFORMATION: n = A,T,C
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(592)
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Percent Similarity:
Best Local Similarity:
Query Match:
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PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR PRIOR PRIOR NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR FILING DATE: 2000-03-3

PRIOR FILING DATE: 1909-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28
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PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR PELICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 30054, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827,129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
                                          NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FeatSEQ for Windows Version 4.0
SEQ ID NO 30054
LENGTH: 592
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LENGTH: 592
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PRIOR FILING DATE: 1999-08-09
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ORGANISM: Human
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OTHER INFORMATION: n = A,T,C
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Best Local Similarity:
Query Match:
                                                             US-10-045-180A-5 (1-44) x US-10-027-632-141529 (1-654)
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Best Local Similarity:
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
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Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 141529
                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows
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NAME/KEY: misc_feature
LOCATION: (1)...(592)
OTHER INFORMATION: n =
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                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                             LENGTH: 654
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/156,358 FILING DATE: 1999-09-28
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Matches:
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Sequence 141529, Application US/10027632

Sequence 141529, Application US/10027632

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/195,218

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/185,363

PRIOR APPLICATION NUMBER: US 60/185,363

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-09-29

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-09-29

PRIOR FILING DATE: 1999-09-29

NUMBER OF SEG ID NOS: 325720

SOFTWARE: FastSEQ for Windows Version 4.0

SEG ID NO 141529

LEMBER: US 60/167,363
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Best Local Similarity:
Query Match:
DB:
Search completed: December 17, 2003, 21:36:01 Job time : 154.128 secs
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US-10-027-632-141529
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TYPE: DNA
ORGANISM: Human
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-MODEL-frame+ P21.model -DEV=xlp
-Q=/cgn2 1/USPTO_spool_p/US10045180/runat_17122003_145025_12578/app_query.fasta_1.860
-Q=/cgn2 1/USPTO_spool_p/US10045180/runat_17122003_145025_12578/app_query.fasta_1.860
-DB=PendIng_Patents_NA_Main_-QFMT=fasta_p -SUPFIX=rnpm -MIRATCH=+0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -WAIRIX=blosum62 -TRANS=+buman40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HRAPSIZES=00 -MINLEN=0 -MAXLEN=200000000
-USER-US10045180_eCGN 1 1 9409_erunat_17122003 145025_12578 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XCAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Ygapop 10.0 ,
Fgapop 6.0 ,
Delop 6.0 ,
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233
1 EPLQARAHEMPAQK
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Listing first 45 summaries
Cgn2_6/ptodata/2/pna/US06_COMB.seq:*
Cgn2_6/ptodata/2/pna/US07_COMB.seq:*
Cgn2_6/ptodata/2/pna/US08_COMB.seq:*
Cgn2_6/ptodata/2/pna/US08_COMB.seq:*
Cgn2_6/ptodata/2/pna/US08_COMB.seq:*
Cgn2_6/ptodata/2/pna/US08_COMB.seq:*
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Cgn2_6/ptodata/2/pna/US086_COMB.seq:*
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Cgn2_6/ptodata/2/pna/US089_COMB.seq:*
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Cgn2_6/ptodata/2/pna/US093B_COMB.seq:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/2/pna/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/pna/PCTUS_COMB.seq.old:*
/cgn2_6/ptodata/2/pna/USO6_COMB.seq:*
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29: /cgm2_6/ptodata/2/pna/US096D_COMB. seq; * 31: /cgm2_6/ptodata/2/pna/US097A_COMB. seq; * 31: /cgm2_6/ptodata/2/pna/US097A_COMB. seq; * 32: /cgm2_6/ptodata/2/pna/US097A_COMB. seq; * 33: /cgm2_6/ptodata/2/pna/US097A_COMB. seq; * 34: /cgm2_6/ptodata/2/pna/US099A_COMB. seq; * 34: /cgm2_6/ptodata/2/pna/US099A_COMB. seq; * 36: /cgm2_6/ptodata/2/pna/US099A_COMB. seq; * 37: /cgm2_6/ptodata/2/pna/US09A_COMB. seq;
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Result No.

Score

Query Match Length

DB

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US-10-170-235-6564 US-10-013-770-2 US-10-045-180A-2 US-10-013-770-1 US-10-045-180A-1

8 610 8 610 8 610 8 610

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 1, Appli
Sequence 1, Appli
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8 9094, Ap
3181, App
3181, App
2 1156, App
2 772, App
2 10452, A
2 10452, A
3 10560, Ap
3 1060, Ap

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Best Local Similarity:
Query Match:
DB:
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US-10-013-770-2
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Sequence 2, Application US/10013770

GENERAL INFORMATION:
APPLICANT: GENSET SA
COMPOSITION CONTAINING SAME AND DIAGNOSTIC AND THERAPEUTIC APPLICATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 GlnAspValValIleTyrPheSerGlyAspAspSerCysSerLeuGlnValProGlySer 40
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                                                                                                                                                                                                                                                                                                                                                                                            CITY: San Diego
STATE: California
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Indels:
Gaps:
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/013,770
FILING DATE: 10-Dec-2001
PRIOR APPLICATION DATA:
APPLICATION UNMER: 09/486,580
FILING DATE: <UNKNOWN:
APPLICATION NUMBER: 09/486,580
FILING DATE: <UNKNOWN:
APPLICATION NUMBER: 09/486,580
FILING DATE: <UNKNOWN:
APPLICATION DATA:
APPLICATION NUMBER: 09/486,580
FILING DATE: <UNKNOWN:
APPLICATION NUMBER: 09/486,580
FILING DATE: <UNKNOWN:
ATTORNEY/AGENT INFORMATION:
NAME: Hart, Daniel

REGISTRATION NUMBER: 40,637

GENSET.064C1

ZIP: 92101 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

COUNTRY: USA

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; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC AC
; TITLE OF INVENTION: TRANSCRIPTS, FOR DETECT
; FILE REFERENCE: CLO01380
; CURRENT APPLICATION NUMBER: US/10/170,235
; CURRENT FILING DATE: 2003-03-17
; NUMBER OF SEQ ID NOS: 42514
; SEQ ID NO 6564
; LENGTH: 285
                                                                                                                                                                                                                              RESULT 1
US-10-170-235-6564
; Sequence 6564, Application US/10170235
; GENERAL INFORMATION:
                                                                                                                                                 NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN FOR DETECTING EXPRESSION AND OTHER USES THEREOF
                                               Alignment Scores: Pred. No.:
Percent Similarity:
                                                                                                                         US-10-013-770-2
                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 453 BASE FAIRS
TYPE: NUCLEOTIDE
STRANDEDNESS: DOUBLE
                                                                                                                                               ORGANISM: Homo sapiens SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                 MOLECULE TYPE: CDNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                   TOPOLOGY: LINEAR
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2.15e-22 233.00 100.00%

Length: Matches:

Conservative:

Best Local Similarity: Query Match:
DB:

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US-10-045-180A-2

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US-10-045-180A-5 (1-44) x US-10-045-180A-2 (1-453)
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             Sequence 1, Application US/10013770 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.1 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/10045180A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Chumakov, ilya
TITLE OF INVENTION: Human Defensin Polypeptide Def-x, Genomic DNA and cDNA, Compositi
TITLE OF INVENTION: Containing Them and Applications to Diagnosis and to Therapeutic
FILE REFERENCE: GEN-1001
CURRENT APPLICATION NUMBER: US/10/045,180A
CURRENT FILING DATE: 2001-10-18
PRIOR APPLICATION NUMBER: US 09/486,580
PRIOR FILING DATE: 2000-02-25
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: PCT/FR98/01864
PRIOR APPLICATION NUMBER: FR 97/10823
PRIOR APPLICATION NUMBER: FR 97/10823
PRIOR FILING DATE: 1997-08-29
PRIOR FILING DATE: 1997-08-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bougueleret, Lydie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: (52)..(336)
OTHER INFORMATION: De
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                     109 GAGCCGCTCCAGGCAAGAGCTCATGAGATGCCAGCCAGAAGCAGCCTCCAGCAGATGAC 168
                                                                                                                                                                                 169 CAGGATGTGGTCATTTACTTTTCAGGAGATGACAGCTGCTCTCTTCAGGTTCCAGGCTCA 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 GAGCCGCTCCAGGCAAGAGCTCATGAGATGCCAGCAGAAGCAGCCTCCAGCAGATGAC 168
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                                                                                                           ACAAAGGGCTTG 240
                                                                                                                                              ThrLysGlyLeu 44
                                                                                                                                                                                                                                                                           GluProLeuGlnAlaArgAlaHisGluMetProAlaGlnLysGlnProProAlaAspAsp 20
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                                                                                                                                      US-10-045-180A-5 (1-44) x US-10-013-770-1 (1-4415)
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                                                                                                                                                                                                                  Best Local Similarity:
                                                                                                                                                                                                                                                         Score:
                                                                                                                                                                                                                                                                                                                               US-10-013-770-1
                                                                                                                                                                                                                                      Percent Similarity:
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APPLICATION DATA:
APPLICATION NUMBER: US/10/013,770
FILING DATE: 10-Dec-2001
PRIOR APPLICATION NUMBER: 09/486,580
FILING DATE: <Unknown>
APPLICATION NUMBER: 09/486,580
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hart, Daniel
REGISTRATION NUMBER: 40,637
REFERENCE/DOCKET NUMBER: GENSET.064C1
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                          3463 GAGCCGCTCCAGGCAAGAGCTCATGAGATGCCAGCCCAGAAGCAGCCTCCAGCAGATGAC 3522
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TITLE OF INVENTION: HUMAN DEFENSIN DEF-X GENE AND DNAC
COMPOSITION CONTAINING SAME AND DIAGNOSTIC AND
THERAPEUTIC APPLICATIONS
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: LINEAR MOLECULE TYPE: DNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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21 GlnAspValValI1eTyrPheSerGlyAspAspAspSerCysSerLeuGlnValProGly 39
                                                                                   GluProLeuGlnAlaArgAlaHisGluMetProAlaGlnLysGlnProProAlaAspAsp 20
                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
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STATE: California
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STREET: 550 West C Street
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100.00%
89.70%
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4276..4278
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RESULT 4 US-10-013-770-1

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Percent Similarity: Best Local Similarity:

Alignment Scores: US-10-045-180A-2

ENGTH: 453

Query Match:

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RESULT 5
US-10-045-180A-1
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CURRENT FILING DATE: 2001-10-18
PRIOR APPLICATION NUMBER: US 09/486,580
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: PCT/FR98/01864
PRIOR FILING DATE: 1998-08-28
PRIOR APPLICATION NUMBER: FR 97/10823
PRIOR APPLICATION NUMBER: FR 97/10823
PRIOR FILING DATE: 1997-08-29
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APPLICANT: Bougueleret, Lydie APPLICANT: Chumakov, Ilya
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Human Defensin Polypeptide Def-X, Genomic DNA and cDNA, Composit TITLE OF INVENTION: Containing Them and Applications to Diagnosis and to TherapeutiFILE REFERENCE: GEN-100D1
                                                       NAME/KEY: misc feature
LOCATION: (1836)..(1874)
OTHER INFORMATION: Exon
FEATURE:
                                                                                                                                    FEATURE:
NAME/KEY: misc feature
LOCATION: (1780)...(1780)
OTHER INFORMATION: n = a,
                      NAME/KEY: misc feature
LOCATION: (1875)..(188
                                                                                                                                                                                                    NAME/KEY: TATA signal LOCATION: (1758)...(1767) OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                  NAME/KBY: misc feature LOCATION: (1150)...(1150) OTHER INFORMATION: n = a
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LOCATION: (1111)...(1111)
OTHER INFORMATION: n = a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (970)..(970)
OTHER INFORMATION: n = a,
FEATURE:
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LOCATION: (670)...(670)
OTHER INFORMATION: n =
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NAME/KEY: misc feature
LOCATION: (143)...(143)
COTHER INFORMATION: n =
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TYPE: DNA
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NAME/KEY: misc_feature
LOCATION: (85)..(85)
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LOCATION: (1)..(4415)
     ION: (1875)..(1880)
INFORMATION: splice donor site
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                  Alignment Scores: Pred. No.:
                                                                   US-10-045-180A-1
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                                                                                  LOCATION: (4374)...
OTHER INFORMATION:
                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY:
                                                                                                                                                  LOCATION: (4274)..(4276)
OTHER INFORMATION: Translation termination codon
                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (4164)..(4379)
OTHER INFORMATION: Exon
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LOCATION: (4161)..(4163)
OTHER INFORMATION: splice
                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature LOCATION: (4123)...(412)
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LOCATION: (3578)...(3583)
OTHER INFORMATION: splice
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LOCATION: (3394)..(3577)
OTHER INFORMATION: Exon 2
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LOCATION: (2186)..(2186)
OTHER INFORMATION: n = a
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LOCATION: (2133)..(2133)
OTHER INFORMATION: n = a,
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                                                                                                                   NAME/KEY:
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LOCATION: (4274)..(427
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OTHER INFORMATION: splice
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LOCATION: (2710)..(2780)
OTHER INFORMATION: L1 fragment
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LOCATION: (2155)..(2335)
OTHER INFORMATION: Alu i
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OTHER INFORMATION: n = a,
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OTHER INFORMATION: n = a
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OTHER INFORMATION: n = a,
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LOCATION: (2367)..(236
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(4374)..(437
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Matches:
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RESULT 7
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; ORGANISM: Human
US-09-947-907-9094
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DB:
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Best Local Similarity:
              APPLICANT: BONAZZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: UCLEIC ACID MOLECULES ENCODING H
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLOOO116
CURRENT APPLICATION NUMBER: US/60/160, 203
CURRENT FILING DATE: 1999-10-19
NUMBER OF SEG ID NOS: 6374
SOFTMARE: FastSEQ for Windows Version 4.0
SEG ID NO 825
                                                                                                                                                                                                               Sequence 825, Application US/60160203 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 9094
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: COLLECTION OF CODING REGION SINGLE

TITLE OF INVENTION: UUCLECTIDE POLYMORPHISM (CSNPS) LOCATED ON EACH OF THE HUMAN

TITLE OF INVENTION: CHROMOSOMES, METHODS OF DETECTION, AND USES THEREOF

FILE REFERENCE: CL000896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 21266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/947,907
CURRENT FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
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LENGTH: 610
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Indels:
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| Sequence 156, Application US/60160203
| GENERAL INFORMATION:
| APPLICANT: BONAZZI, VIVIEN
| TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
| TITLE OF INVENTION: USES THEREOF
| TITLE OF INVENTION: USES THEREOF
| FILE REFERENCE: CLOOD116
| CURRENT APPLICATION NUMBER: US/60/160,203
| CURRENT APPLICATION NUMBER: US/60/160,203
| CURRENT FILING DATE: 1999-10-19
| NUMBER OF SEQ ID NOS: 6374
| SOFTMARE: FASTSEQ for Windows Version 4.0
| SEQ ID NO 156
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Best Local Similarity:
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Query Match:
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; ORGANISM: HUM
US-60-160-203-825
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3181
LENGTH: 610
TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: Bonazzi, Vivien
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED I
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED I
TITLE REFERENCE: CL000164
FILE REFERENCE: CL000164
CURRENT APPLICATION NUMBER: US/60/169,840
CURRENT FILING DATE: 1999-12-09
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Matches:
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APPLICANT: Greenberg, Simon
APPLICANT: Rabkin, Steven
APPLICANT: Wang, Yu
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMA
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000687
CURRENT APPLICATION NUMBER: US/60/212,664
CURRENT APPLICATION NUMBER: US/60/212,664
CURRENT FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 636
SOFTWARE: FASTSEQ for Windows Version 4.0
US-60-171-481-272/c
; Sequence 272, Application US/60171481
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
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Best Local Similarity:
                                                                RESULT 11
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LOCATION: (1)...(111999)
OTHER INFORMATION: n = A
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ORGANISM: HUMAN
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ORGANISM: HUMAN
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                                                                                                          21 GlnAspValVallleTyrPheSerGlyAspAspSerCysSerLeuGlnValProGly 39
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Greenberg, Simon
Pahkin, Steven
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; Sequence 777, Application US/60171481
; GENERAL INFORMATION:
APPLICANT: BONAZZI, VIVIEN
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USCLEIC ACID MOLECULES ENCODING HUM;
TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000169
; CURRENT APPLICATION NUMBER: US/60/171,481
; CURRENT FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 1898
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 777
; Sequence 10452, Application US/09321214; GENERAL INFORMATION:
                                         RESULT 13
US-09-321-214-10452/c
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Best Local Similarity:
Query Match:
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TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLO00169
CURRENT APPLICATION NUMBER: US/60/171,481
CURRENT FILING DATE: 1999-12-22
NUMBER OF SEQ ID NOS: 1988
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 272
LENGTH: 345
TYPE: DNA
NCRANISM: Human
US-60-171-481-272
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US-60-171-481-777/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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                                                                                                                        pGlnAspValValIleTyrPheSerGlyAspAspSerCysSerLeuGlnValProGly 39
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                                                                                                 CCAGGATGTGGTCATTTACTTTTCAGGAGATGACAGCTGCTCTTCTTCAGGTTCCAGGT 102
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RESULT 14
US-09-516-335-10452/c
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Best Local Similarity:
Query Match:
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Pred. No.:
                                                                                                                                            APPLICANT: Garcia, Veronica
APPLICANT: Giedt, Gretchen
APPLICANT: Jones, Aron
APPLICANT: Jones, Leni
APPLICANT: Jones, Lee
APPLICANT: Kita, David
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CURRENT APPLICATION NUMBER: US/09/321,214
CURRENT FILING DATE: 1999-05-26
EARLIER APPLICATION NUMBER: US 60/088,041
EARLIER FILING DATE: 1998-06-02
NUMBER OF SEQ ID NOS: 31906
SOFTWARE: RastSeQ for Windows Version 3.0
SEQ ID NO 10452
                                                                                                                                                                                                                                                                                                                               APPLICANT: Arterburn, Matthew
APPLICANT: Asghari, Vida
APPLICANT: Damavandi, Simin
APPLICANT: Dickson, Mark
APPLICANT: Drake, Jim
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APPLICANT: Leshkowitz, Dena
APPLICANT: Kita, David
APPLICANT: Ford, John
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APPLICANT: Labat, I
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APPLICANT: Dickson, Mark
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: Labat, Ivan
: Laroya, Mimi
: Lomelli, Michelle
: Nelken, Sarah
: Nguyen, Kody
: Nguyen, Kynne
: Nguyen, Lynne
: Nguyen, Phuong
: Nguyen, Margie
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Faulkner, Brandy
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CURRENT APPLICATION NUMBER: US/09/516,335
CURRENT FILING DATE: 2000-03-01
FEARLIER APPLICATION NUMBER: 09/321,214
FEARLIER FILING DATE: 1999-05-26
FEARLIER APPLICATION NUMBER: 60/088,041
FEARLIER FILING DATE: 1998-06-02
FILING DATE: 1998-06-02
FULL BROWNER: FASTSEQ for Windows Version 3.0
SEQ ID NO 10452
FEARLIER FILING DATE: 1980-06-02
FEARLIER FILING DATE: 1998-06-02
FEARLIER FILING DATE: 19
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US-09-733-811-10452/c
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 740CIP
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APPLICANT: Raisi, Fariba
APPLICANT: Randhwa, Gurpreet
                                                                         PPLICANT
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APPLICANT: Tran, Lien
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ORGANISM: Homo sapiens
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Smythe, Ashleigh
Labat, Ivan
Laroya, Mimi
Lomelli, Mich
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Jomek, Leni
Jones, Lee
Kita, David
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Giedt, Gretchen
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Damavandi, Simin
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Faulkner, Brandy
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Drake, Jim
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Asghari, Vida
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APPLICANT: Randhwa, Gurpreet
APPLICANT: Sidhu, Navjiwan
APPLICANT: Smith, Benjamin
APPLICANT: Smith, Benjamin
APPLICANT: Smythe, Ashleigh
APPLICANT: Trach, Joe
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: NOWER: US/09/733,811
CURRENT APPLICATION NUMBER: US/09/733,811
CURRENT FILING DATE: 2000-12-08
PRIOR FILING DATE: 1990-05-26
PRIOR APPLICATION NUMBER: 09/321,214
PRIOR FILING DATE: 1998-06-02
NUMBER OF SEQ ID NUMBER: 60/088,041
PRIOR FILING DATE: 1998-06-02
NUMBER OF SEQ ID NOS: 31906
SOFTWARE: FRAETSEQ for Windows Version 3.0
SEQ ID NO 10452
LENGTH: 338
TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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Search completed: December 17, 2003, 21:11:01 Job time: 2320.08 secs
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                                                                                                                                        200 CAGGAAGTGGTTGATTCCTTTGCATGGGÁTGAAAGAGCTCCTCTTCÁGGTTTCAGGCTCÁ 141
                                                                                                     41 ThrLysGlyLeu 44
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Nguyen, Kody
Nguyen, Lynne
Nguyen, Phuong
Nogra, Margie
Palencia, Servando
Raisi, Fariba
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120.00
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Matches:
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Result
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Maximum DB seq length: 2000000000
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-Q=/cgn2 1/USPTO_spool_p/US10045180/runat_17122003_145024_12553/app_query.fasta_1.860
-DB=Issued_patents_NA -QPMT_fastap -SUPFIX=rni -MINMATCH=0.1 -LOOPCI=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -WATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE-LOCAL -OUTFMT=pto -NORM=ext -HBAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10045180 @GGN 1 193 @runat 17122003 145024 12553 -NCPU=6 -ICPU=3
-NO MMAD -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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1: /cgn2_6/ptcdata/

2: /cgn2_6/ptcdata/

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by analysis of the total
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/cgn2 6/ptodata/2/ina/5B_COMB.seq:*
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US-09-309-487-13
US-09-309-487-13
US-09-309-487-25
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Sequence 2, Appli
Sequence 1, Appli
Sequence 6, Appli
Sequence 1198, Ap
Sequence 28, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 25, Appl
                                                                                                                                                                                                                                                                                                                                            Description
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TITLE OF INVENTION:
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                             TYPE: NUCLEOT STRANDEDNESS: TOPOLOGY: LIN
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## ALIGNMENTS

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US-09-486-580A-2
Sequence 2, Application US/09486580A
Patent No. 6329340
GENERAL INFORMATION:
APPLICANT: GENST SA
APPLICANT: GENST SA
ITILE OF INVENTION: THERAPEUTIC ADDITIONS
INTHE OF INVENTION: THERAPEUTIC APPLICATIONS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 550 West C Street
CITY: San Diego
STATE: California
COUNTRY: USA
ILP: 92101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: DATA: DATA:
APPLICATION NUMBER: US/09/486,580A
FILING DATA: FEBRUARY 25, 2000
ATTORNEY/AGENT INFORMATION:
RESTERENCE/DOCKST NUMBER: GENSET.064C1
INFORMATION CON RESPONSED FOR SEQUENCE CHARACTERISTICS:
LENGTH: 453 BASE FAIRS
TYPE: NUCLEOTIDE
STRANDEDNESS: DOUBLE
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
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RESULT 2
US-09-486-580A-1
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DB:
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Best Local Similarity:
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                                                                                                                                                                                                       NAME: Hart, Daniel
REGISTRATION NUMBER: 40,637
REFERENCE/DOCKET NUMBER: GENS
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4415 BASE PAIRS
TYPE: NUCLECTIOE
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APPLICANT: GENEST SA
TITLE OF INVENTION: CU
TITLE OF INVENTION: CT
TITLE OF INVENTION: TH
NUMBER OF SEQUENCES: 6
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                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/486,580A
FILING DATE: FEBRUARY 25, 2000
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: SAN Diego CITY: San Diego CTATE: California
            FEATURE:
NAME/KEY:
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ADDRESSEE: Knobbe, Marten:
STREET: 550 West C Street
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ORGANISM: Hom
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                                                           NAME/KEY:
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Applic
Patent No. 5641497
                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: JOHNSON, Philip S.
REGISTRATION NUMBER: 27,200
REFERENCE/DOCKET NUMBER: CH-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                            TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
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NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No.
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bevins, Charles L.
APPLICANT: Jones, Douglas E.
TITLE OF INVENTION: Gastrointestinal Defensin Peptides,
TITLE OF INVENTION: CDNA Sequences, Methods for Production
                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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LOCATION:
                                        LENGTH: 452 base pair
TYPE: nucleic acid
STRANDEDNESS: single
NAME/KEY:
                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
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                            TOPOLOGY:
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Matches:
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; IMMEDIATE SOURCE:
; LIBRARY: GENBAI
; CLONE: g181546
US-09-016-434-1198
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US-09-016-434-1198
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Query Match:
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APPLICANT: Janice Au-Young

APPLICANT: Jeffrey J. Seilhamer

APPLICANT: Jeffrey J. Seilhamer

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

TITLE OF INVENTION: PATHWAY GENE EXPRESSION

NUMBER OF SEQUENCES: 1490

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1198, Application US/09016434 Patent No. 6500938
                                                                                                                                         REFERENCE/DOCKET NUMBER: PATELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1198
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                     TOPOLOGY:
                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                          LENGTH:
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
; Sequence 28, Application US/09967808
; Patent No. 6514727
; GENERAL INFORMATION:
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                                         US-09-967-808-28
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Query Match:
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US-09-309-487-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 28
LENGTH: 243
TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Yuan, Jun
APPLICANT: Yuan, Jun
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
FILE REFERENCE: P-UC 3095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/309,487
CURRENT FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
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Best Local Similarity:
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                                                                                                                                                                                                                                  APPLICANT: Selsted, Michael E.
APPLICANT: Selsted, Michael E.
APPLICANT: Tang, Yi-Quan
APPLICANT: Yuan, Jun
APPLICANT: Yuan, Jun
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
FILE REFERENCE: P-UC 3095
CURRENT APPLICATION UNMBER: US/09/309,487
CURRENT FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15, Application US/09309487 Patent No. 6335318
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (7)...(237)
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LENGTH: 243
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SEQ ID NO 15
LENGTH: 495
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                                                                                                            PEATURE:
NAME/KEY: CDS
LOCATION: (90)..(320)
                                                                                                                                                            ORGANISM: Macaca mulatta
                                                                                                                                                                             TYPE: DNA
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Tang, Yi-Quan
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Matches:
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DB:
                                                                    US-09-309-487-13
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Best Local Similarity:
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GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Tang, Yi-Quan
                                        Sequence 13, Application US/09309487 Patent No. 6335318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Selsted, Michael
APPLICANT: Tang, Yi-Quan
APPLICANT: Yuan, Jun
APPLICANT: Ouellette, Andre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15, App
Patent No. 65147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods TITLE OF INVENTION: Same
                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: CDS
LOCATION: (90)..(320)
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LENGTH: 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 65147
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Selsted, Michael E. APPLICANT: Tang, Yi-Quan APPLICANT: Yuan, Jun APPLICANT: Ouellette, Andre J.
                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using TITLE OF INVENTION: Same FILE REFERENCE: P.UC 3095 CURRENT APPLICATION NUMBER: US/09/967,808 CURRENT FILLING DATE: 2001-09-26 PRIOR APPLICATION NUMBER: US/09/309,487 PRIOR FILLING DATE: 1999-05-10
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CURRENT FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
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APPLICANT: Ouellette, Andre J.
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                                                                                                                                            NAME/KEY: CDS
LOCATION: (95)..(325)
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Query Match:
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US-10-045-180A-5 (1-44) x US-08-158-189-4 (1-424)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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APPLICATION NUMBER:
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REGISTRATION NUMBER: 27,200
REFERENCE/DOCKET NUMBER: CH
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ZIP: 19103
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; TYPE: DNA; ORGANISM: Macaca mulatta US-09-967-808-25
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US-09-967-808-25
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US-09-309-487-25
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APPLICANT: Selsted, Michael E.
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Sequence 25, Appr-
No. 6335318
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                                                                    SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 25
                                                                                                 APPLICANT: Selsted, Michael E.
APPLICANT: Tang, Yi-Quan
APPLICANT: Yuan, Jun
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using
TITLE OF INVENTION: Same
FILLE REFERENCE: P-UC 3095
CURRENT APPLICATION NUMBER: US/09/967,808
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US/09/309,487
PRIOR FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
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CURRENT APPLICATION NUMBER: US/09/309,487
CURRENT FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Yuan, Jun
APPLICANT: Ouellette, Andre J.
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CURRENT FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 24, Application US/09309487 Patent No. 6335318
                            Sequence 24, Application Patent No. 6514727 GENERAL INFORMATION:
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APPLICANT: Selsted, Michael E.
APPLICANT: Tang, Yi-Quan
APPLICANT: Yuan, Jun
APPLICANT: Ouellette, Andre J.
APPLICANT: Selsted, Michael E. APPLICANT: Tang, Yi-Quan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same FILE REFERENCE: P-UC 3095
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APPLICANT: Yuan, Jun
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using
TITLE OF INVENTION: Same
FILE REFERENCE: P-UC 3095
CURRENT APPLICATION NUMBER: US/09/967,808
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US/09/309,487
PRIOR FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 24
LENGTH: 2525
TYPE: DNA
TYPE: DNA
US-09-967-808-24
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Search completed: December 17, 2003, 14:54:02 Job time : 46 secs
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Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp
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-Q=/Ggn2_1/USPTO_spool_p/US10045180/runat_17122003_145023_12528/app_query.fasta_1.860
-Q=/Ggn2_1/USPTO_spool_p/US10045180/runat_17122003_145023_12528/app_query.fasta_1.860
-Q=/Ggn2_1/USPTO_spool_p/US10045180/runat_1-LOOPCT=0.1-LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MAXRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-DUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXIEN=200000000
-USER=US10045180_GCGN 1 1 5283 @Funat 17122003 145023 12528 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPB_LOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query

#### Result No. 85.5 100.0 453 100.0 4415 100.0 4415 100.0 128544 83.2 163604 83.2 188604 52.9 271979 52.9 271979 46.6 337 46.6 435 44.6 435 44.6 435 44.8 1260 44.0 494 Match 44.0 42.9 42.4 42.4 44.0 433 1260 194 504 3003 3003 3046 3400 242829 67979 485 Length 109 316 448 451 464 498 498 5149 5149 5149 7110 37110 BB AC116559 AC116558 AC098442 AC028185 AF188268 AF184160 AF184159 HUMDEFJA HUMDEFB HSDEFB HSDEF3 BD028213 HSHP1 BD174049 HUMDEFIAA BD023843 AX40575 BC027917 AF188270 RABDNP4A BD128611 I32861 RNU50356 RNU16684 RNU16683 RRU50354 RNU50353 RNU50355 AC114391 AC114399 196061 AF119902 BD174050 HUMNTRI A98571 BD074746 I32862 I32863 AC116559 Papio anu AC116558 Papio anu AC1059842 Rattus no AC128185 Rattus no AC128185 Rattus no AC128185 Macaca mu AF184159 Macaca mu AF184159 Macaca mu AF184159 Macaca mu OS0356 Rattus norv U16683 Rattus norv U50353 Rattus norv U50353 Rattus norv U50357 Rattus norv U50358 Rattus norv U50359 Rattus norv AC113099 Mus muscu AF188270 Macaca mu AC113099 Mus muscu AF188270 Macaca mu M64601 Cryctolagus BD128611 Method fo I32861 Sequence 44 I32863 Sequence 44 I32863 Sequence 44 I32863 Sequence 65 I32878 Sequence 61 M21131 Homo sapien BD023843 Sequence AX405718 Sequence AX588765 Sequence BC027917 Homo sapi I30337 Sequence 5 A98571 Sequence 2 BD074746 Human def A98570 Sequence 1 BD074745 Human def AF238378 Homo sapi BD028213 Sequence X52053 Human mRNA Af119902 Homo sap BD174050 Method of BD174049 Method of L12691 Human neutr M26602 Human defen Description

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L Patent: JP 2001514264-A 2 11-SEP-2001;

GENSET

OS Homo sapiens (human)

PN JP 2001514264-A/2

PD 11-SEP-2001

PF 28-AUG-1998 JP 2000508701

PF 28-AUG-1998 JP 2010508701

PR 29-AUG-1997 FR 97/10823

PI LYDIE BOUGUELERET,ILYA SHMACOV

PC C07X14/435,A01N43/50,A01N63/00,A61K7/00,A61K38/00,A61P2

PC A61P35/00,

PC A61P35/00,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N15/0

PC A61P31/02,C07K16/18,C12N1/15,A61K37/02,C12N15/00

C12P21/02,C12P1/08,G12Q1/68,G01N33/53,A61K37/02,C12N15/00 CC

Strandedness: Double,

CC Topology: Linear;
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BOUGUELERET LYDIE (FR); CHUMAKOV ILYA (FR)
LOGALERET LYDIE (FR); CHUMAKOV ILYA (FR)
LOGALERET LYDIE (FR); CHUMAKOV ILYA (FR)
LOGALERET LYDIE (FR); CHUMAKOV ILYA (FR)
                                                                                                                                                                                                                                                            Bougueleret.L. and Shmacov,I.

Human defensin polypeptide Def-X, genome DNA and cDNA, composition containing the same, and application to diagnosis and remedy Patent: JP 2001514264-A 2 11-SEP-2001;
                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 453)
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Sequence 2 from Patent WO9911663.
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29-AUG-1997 FR 97/10823
LYDIE BOUGDELERET, ILYA SHMACOV
C07K14/435,A01N43/50,A01N63/00,A61K7/00,A61K38/00,A61P29/00,
                                                                           A61P37/02,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N15/09, PC
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/mol_type="genomic DNA"
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                                US-10-045-180A-6 (1-31) x A98570 (1-4415)
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                                                                                                                                                                                                                                                                      Bougueleret,L. and Chumakov,I.
HUMAN DEFENSIN DEF-X, GENE AND DNAG, COMPOS:
AND DIAGNOSTIC AND THERAPEUTIC APPLICATIONS
PAtent: WO 9911653-A 1 11-MAR-1999;
BOUGUELERET LYDIE (FR); CHUMAKOV ILYA (FR)
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1 from Patent A98570
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/mol_type="genomic DNA"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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GENORY
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Human defensin polypeptide Def-X,
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Mammalia; Eutheria; Primates;
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ATCCTTGGTGAACGCTACCCAATCTGCTGCTAC 4273
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11-SEP-2001
28-AUG-1998 JP 2000508701
29-AUG-1997 FR 97/10823
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Human defensin polypeptide Def-X, genome DNA and cDNA,
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C07K14/435,A01N43/50,A01N63/00,A61K7/00,A61K38/00,A61P29/00,
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                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
1109 c 912 g 125
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3406. .3408
4276. .4278.
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Mismatches:
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COMMENT

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the

assembly was confirmed by restriction digest.

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REFERENCE
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AF238378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (06-JUL-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany 6 (Dases 1 to 128544)
Lagemann, D. and Platzer, M.
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4 (bases 1 to 128544)
Genome Sequencing Center Jena.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polley,A., Baumgart,C., Blechschmidt,K., Dette,M.D., Jahn,N., Menzel,U., Reichwald,K., Schilhabel,M.B., Schudy,A., Taudien,S., Wen,G., Schutte,B., Malik,M., Peng,J.Hong., McCray,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (02-APR-2003) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (10-NOV-2000) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany
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Homo sapiens chromosome 8 clone SCb-561b17 map p22-p21, complete
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Lagemann, D. and Platzer, M.
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Direct Submission
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1 (bases 1 to 128544)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequencing vector: pUC18; 100% of reads chemistry: Dye-terminator Big Dye; 100% of re Assembly program: Phrap; version 0.990329 Consensus quality: 127999 bases at least Q40 Consensus quality: 128330 bases at least Q30 Consensus quality: 128544 bases at least Q20 Quality coverage: 11.05x
                                                                                                                                                                                                         Center project name: H370
Center clone name: SCb-561b17
                                                                                                                                                                                                                                                    Web site: http://genome.imb-jena.de/
Contact: gscj-submit@genome.imb-jena.de
                                                                                                                                                                                                                                                                                                                                      Center: Insitute of Molecular Biotechnology Center code: IMB
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FEATURES
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This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
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                                                                                                                                                                       /note="single stranded/single chemistry region" 56028 ...56165 /note="single stranded/single chemistry region" 57952 ...58060
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53612. .53926
/note="single stranded/single chemistry region"
53674. .53677
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47899. .47900
/note="low quality region"
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45815. .45872
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45824. .45872
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/db_xref="taxon:9606"
/chromosome="8"
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'mol_type="genomic DNA"
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21 IleLeuGlyGluArgTyrProIleCysCysTyr 31

Alignment Scores: Pred. No.: Score: Score: Percent Similarity: Best Local Similarity Query Match: DB: US-10-045-180A-6 (1-3 Qy 1 TleCysH               Db 62550 ATCTGCC	misc_feature misc_feature misc_feature	o financia	eature eature eature	unsure unsure misc_feature misc_feature misc_feature unsure unsure unsure unsure unsure unsure	misc_feature misc_feature misc_feature misc_feature misc_feature misc_feature unsure unsure misc_feature	H I
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AUTHORS
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AC116559
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US-10-045-180A-6 (1-31) x AC116559 (1-163093)
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* consists of 3 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* the accession number will be preserved.
* 6315: contig of 6315 bp in length
* 6416 16704: contig of inlength
* 16804: gap of unknown length
* 16804: gap of unknown length
* 16804: gap of unknown length
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Submitted (30-MAY-2003) Department Of Chemistry And Biochemistry,
Thiversity Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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Direct Submission
Submitted (29-MAR-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC116559 163093 bp DNA linear HTG 30-MAY-2003
Papio anubis clone rp41-339c10, WORKING DRAFT SEQUENCE, 3 ordered
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1 (bases 1 to 163093)
Xu,W., Hua,A., Eichler,E. and Roe,B.A.
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W., Hua,A., Eichler,E. and Roe,B.A.
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                                                                                                                                                                                                                                                                           /organism="Papio anubis"
/mol_type="genomic DNA"
/db_xref="taxon:9555"
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/clone lib="RPCI - 4
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Butheria; Primates; Catarrhini; Cercopithecidae;
                                       1.08e-11
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                                                                                              Length:
Matches:
Conservative:
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46065 t 224 others
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CysHisCysArgValLeuTyrCysIlePheGlyGluHisLeuGlyGlyThrCysPheIle

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RESULT 7
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Best Local Similarity:
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US-10-045-180A-6 (1-31) x AC116558
                                                          Query Match:
                                                                                                                        Score:
                                                                                                                                             Pred. No.:
                                                                                                                                                              Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xu,W., Hua,A., Eichler,E. and Roe,B.A.
Direct Submission
Submitted (29-MAR-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTG; HTGS PHASE2; HTGS DRAFT.
Papio anubis (olive baboon)
Papio anubis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 188604)
Xu, W., Hua, A., Eichler, E. and Roe, B.A.
Papio anubis BAC Clone rp41-273g19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OK 73019, USA
On May 15, 2003 this sequence version replaced gi:28173120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (11-JUN-2003) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OK 73019, USA
3 (bases 1 to 188604)
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC116558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Department Of Chemistry And Biochemistry The University Of Oklahoma
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                       by the finished sequence as soon as it is available the accession number will be preserved.

1 6057: contig of 6057 bp in length
6058 6157: gap of unknown length
6158 188604: contig of 182447 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence will be replaced
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W., Hua, A., Eichler, E. and Roe, B.A.
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                                                                                                                                                                                                                        /clone="rp41-273g19"
/clone lib="RPCI - 41
41769 c 40796 g :
                                                                                                                                                                                                                                                                                       /organism="Papio anubis"
/mol_type="genomic DNA"
/db_xref="taxon:9555"
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40796 g 52555 t 100
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                                                          Conservative: Mismatches: Indels:
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                                                                                           JOURNAL
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CCE 1 (basee 1 to 271979)

RS Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Are J.R., Ayele, M., Banks, T., Alsbrooke, S.L., Amaratunge, H.C., Are J.R., Ayele, M., Banks, T., Alsbrooke, S.L., Amaratunge, H.C., Are J.R., Ayele, M., Banks, T., Alsbrooke, S.L., Amaratunge, H.C., Are J.R., Brown, M., Bryant, N.P., Barbaria, J., Benton, J., Binakenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Erown, E., Berown, M., Bryant, N.P., Buhay, C., Barch, P., Barketh, C., Burrell, K.L., Bydd, N.C., Chen, G., Chen, G., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Davila, R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Lare, R., Chen, S., Durbin, K.J., Delgado, J., Garcia, A., Garrell, J., Decter, P., Frantz, P., Bella, S., Leath, R., Lare, R., Gabisi, A., Garcia, A., Garrer, T., Garra, N., Gill, R., Garris, M., Guaratune, P., Hale, S., Hamilton, K., Haris, T., Ferraguto, D., Flagy, N., Ford, J., Forter, P., Frantz, P., Gabisi, A., Garris, M., Haris, M., Haris, M., Haris, J., Jackson, E., Kelly, S., Khan, U., King, L., Korvah, J., Jackson, E., Homson, R., Holloway, C., Hollins, B., Jacobson, B., Jia, Y., Johnson, R., Jolives, M., Holloway, C., Hollins, B., Jacobson, B., Kareshi, A., Landry, N., Leal, B., Lewis, L.C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lucier, A., Lucier, R., Martindale, A., Martinez, E., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., McLeod, M.P., Wassey, M., Walley, N., Okwuon, G., Orgh, M., Okwuon, G., Orgh, M., Okwuon, G., Orgh, M., Okwuon, G., Orgh, M., Okwuon, G., Wallians, M., Satery, G., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Stone, H., Stone,
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
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Rattus norvegicus clone CH230-2J1,
3 unordered pieces.
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                         Submitted (23-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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*** SEQUENCING IN PROGRESS ***,
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Submitted (13-NOV-2002) Human Genome Sequencing Center, Department JOURNAL of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 13, 2002 this sequence version replaced gi:23664583.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome Center code: BCM

Center Code: BCM

Center clone name: CH230-231

Consensus quality: 24990 bases at least Q40
Consensus quality: 24990 bases at least Q40
Consensus quality: 24990 bases at least Q40
Consensus quality: 24922 bases at least Q40
Consensus quality: 24322 bases quality: 24322 bases quality: 24322 bases quality: 24324
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/cenbank\_draft\_data.h NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved /note="wgs\_end\_extension clone\_end:Sp6" 2826 \_\_4261 150206. .150798
/note="clone\_boundary
clone\_end:T7 /note="wgs\_end\_extension clone\_end:Sp6" olo2\_e076 /note="wgs\_end\_extension clone\_end:T7" 266939.end\_sequence:BH288135" /db\_xref="taxon:10116" /clone="CH230-2J1" 1. .27197 Socation/Qualifiers note="clone\_boundary" mol\_type="genomic DNA" organism="Rattus norvegicus" one\_end:Sp6 .1234 268032: contig of 268032 bp in length 268132: gap of unknown length 270509: contig of 2377 bp in length 270609: gap of unknown length 271979: contig of 1370 bp in length. sequence:BH288134" .9978 .4181 .268032 draft data.html).

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RESULT 9
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ORIGIN
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         Allen, C., Allen, H., Alsbrooks, S., Amin, A., Aguiano, D.,
Anlen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalsbechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Bayalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Baswalo, K., Blair, J., Blarkenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chen, Z., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davia, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Diny, Y., Dinh, H., Divya, K.,
Delgado, O., Denson, S., Deramo, C., Diny, Y., Dinh, H., Divya, K.,
Draper, H., Dayas, E., Geer, K., Gill, R., Garcia, A., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
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Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M.,
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Liu, J., Liu, W., Liu, Y., Lobow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
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Kowais, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
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Mayan, M., Martin, R., Perez, A., Perez, L., Pfannsch, R.,
Pal, S., Shen, H.,
Sanders, K., Sanders, S., Shen, H.,
San
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (22-SEP 2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Sep 22, 2002 this sequence version replaced gi:21908787.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequenting reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Worley, K.C.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html)
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html)
(NOTE: This sequence may represent more than one clone.

NOTE: This is a 'working draft' sequence. It currently
consists of 4 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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Center clone name: GYBD

Center clone name: GH230-30N20

Center clone name: CH230-30N20

Assembly program: Phrap; version 0.990329

Consensus quality: 240138 bases at least Q40

Consensus quality: 244747 bases at least Q30

Consensus quality: 24771 bases at least Q20

Consensus quality: 24771 bases at least Q20

Estimated insert size: 272390; sum-of-contigs estimation Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
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                                                                                                           1. .301130
/mol_type="genomic DNA"
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                                                                          organism="Rattus norvegicus"
                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                      3552: contig of 3552 bp in length
3652: gap of unknown length
16658: contig of 13006 bp in length
16758: gap of unknown length
296490: contig of 279732 bp in length
296590: gap of unknown length
301130: contig of 4540 bp in length.
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RESULT 10
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DB:
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Submitted (20-SEP-1999) Pathology, Irvine, CA 92697, USA Location/Qualifiers
                                                                                                                                                                                        1 (bases 1 to 347)
Tang,Y.Q., Yuan,J., Miller,C.J. and Selsted,M.E.
Tsolation, characterization, cDNA cloning, and antimicrobial
properties of two distinct subfamilies of alpha-defensins fro
                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                          Macaca mulatta
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                                                     3 (bases 1 to 347)
Selsted, M.E.
                                                                               Rhesus myeloid defensins 
Unpublished
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                                           Direct Submission
                                                                                                            Selsted, M.E.
                                                                                                                                                              rhesus macaque leukocytes
Infect. Immun. 67 (11), 6139-6144 (1999)
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clone_end:T7
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clone_end:Sp6"
complement(8004. 8619)
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1631. 3:55
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                                                                                                                                                                                                                                                       Zhao, C., Nguyen, T. and Lehrer, R.I. Direct Submission Submitted (10-SEP-1999) Medicine,
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Macaca mulatta alpha-defensin IA (MNP1A) mRNA, complete
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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VSLAWDESLAPKDSVPGLRKNMACYCRIPACLAGERRYGTCFYLGRVWAFCC"
102 c 94 g 75 t
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      /Godon_start=1
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/db_xref="GI:6409290"
/translation="WRTLAILLAILLVALQAQAEPLQARTDEATAAQEQIPTDNPEVV
VSLAWDESLAPKDGLRKOWACYCRIPACLAGERRYGTCFYLGRVWAFCC"
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/mol_type="mRNA"
/db_xref="taxon:9544"
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/db_xref="GI:6273106"
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/mol_type="mRNA"
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Location/Qualifiers
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AF184159.1 GI:6409287
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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Macaca mulatta alpha-defensin
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LeuGlyGluArgTyrProIleCysCys 30
                         TGCTATTGCAGAATACCAGCGTGCTTAGCAGGAGAACGTCGCTATGGAACCTGCTTCTAC 273
                                            CysHisCysArgValLeuTyrCysIlePheGlyGluHisLeuGlyGlyThrCysPheIle 21
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VSLAWDESLAPKDSVPGLRKNWACYCRIPACLAGERRYGTCFYMGRVWAFCC"
113 c 102 g 97 t
                                                                                                                                                                                                                                                        /product="alpha-defensin 1"
/protein_id="AAF07925.1"
/db_xref="GI:6409288"
                                                                                                                                                                                                                                                                                                                                                         organism="Macaca mulatta"
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51.72%
44.76%
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US-10-045-180A-6 (1-31) x RNU50356 (1-1260)
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RNU16684 494 bp
Rattus norvegicus defensin RatNP-4
U16684
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Submitted (29-FEB-1996) Niaz
Med. Sci., Irvine, CA 92717,
Location/Qualifiers
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Banaiee,N., Yount,N.Y. and Selsted,M.E.
Molecular Characterization of Genes Encoding
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Eukaryota; Metazoa; Chordata;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Norway rat)
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ATGGGAAGAGTCTGGGCATTCTGCTGC
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978. .989
/note="GAA trinucleotide variable number
a 271 c 243 g 374 t
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/mol_type="genomic DNA"
/strain="Sprague Dawley"
/db xref="taxon:10116"
<1. 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="neutrophil defensin"
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             precursor mRNA,
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GI:1041806

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KEYWORDS
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                                       Rattus norvegicus defensin RatNP-3
U16683
U16683.1 GI:1041804
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Rattus norvegicus (Norway rat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yount, N.Y.
Direct Submission
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Mammalia; Eutheria; Rodentia;
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J. Immunol. 155 (9), 4476-4484 (1995)
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                                                                                                                                                                                          TGCTATTGCAGAATCGGAGCCTGTGTTTCTGGAGAACGGCTCACTGGGGCATGTGGTCTC 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Repeat element is not perfect.
analyzed repeat element is identical"
478. .483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="defensin peptide RatNP-4"
358. .400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MRTLTLLITLLLLALHTQAESPQERAKAAPDQDMVMEDQDIFIS
FGGYKGTVLQDAVVKAGQACYCRIGACVSGERLTGACGLNGRIYRLCCR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="bone marrow"
/clone_lib="plasmid, oligo dT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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Job time : 961.963 secs

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AUTHORS
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Submitted (27-OCT-1994) Nannette Y. Yount, Pathology, Submitted (27-OCT-1994) Irvine, CA 92717, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yount, N.Y., Wang, M.S., Yuan, J., Banaiee, N., Ouellette, A.J. and Selsted, M.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rat neutrophil defensins. Precursor structures and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Yount, N.Y.
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                                                                       LeuGlyGluArgTyrProIleCysCys 30
                                                                                                     TGCTCTTGTAGAACCTCAAGCTGTCGTTTTTGGAGAAAAGGCTCTCTGGGGCATGTCGTCTC
                                                                                                                             CysHisCysArgValLeuTyrCysIlePheGlyGluHisLeuGlyGlyThrCysPheIle 21
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                                                                                                                                                                                                                                                                                                                                                                                polypurine GAA sequence.
GAA-motif was repeated 20
repeated 31 times"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
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/db_xref="d1:1041805"
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GTALQDAAVKAGVTCSCRTSSCRFGERLSGACRLNGRIYRLCC"
                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="defensin peptide RatNP-3"
333. .404
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62. .325
                                                                                                                                                                                                                                                                                                                                                                                                                            note="cDNA sequence shown with 24 repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue type="bone marrow"
/clone_lib="plasmid, oligo
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/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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Command line parameters:

-MODEL-frame-p2n.model -DEV=xlp
-Q-/cgn2_1/USPTO_spool_p/US10045180/runat_17122003_145024_12540/app_query.fasta_1.860
-Q-/cgn2_1/USPTO_spool_p/US10045180/runat_17122003_145024_12540/app_query.fasta_1.860
-DB=EST_QFMT=fastap_SUFFIX=rst -MINMATCH=0.1 -LOODFCL=0 -LOODFXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN-10-TMXLEN-2000000000
-USER-US10045180_eCGN 1 6100_exunat_17122003_145024_12540 -NCFU=6 -ICFU=3
-NO_MMAP -LARGEQÜERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Fgapop 6.0 , F
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Copyright (c) 1993 - 2003 Compugen Ltd.
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## 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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31364	-MT00	31414 QV4.	831411 QV4.	QV4		E831405	E831402 QV4.	831398 QV4.	E831397	831396 QV4-	831382 QV4-	831369 QV4-MT00	31314 QV4-MT00	831385 OV4-MT00	E831389 OV4-MT00	334909 IL2	35021 th76		903483 TL2	01500 11.2	F901407 TI.2.	F901251 TI.2.	E831401 OV4	1022826 CM0	831426 OV4	274523 xv30h12.x	831404 OV4-MT00	831399 OV4	CM4-MT02	903426 II.2-MT01	028909 PM3-MT02	993374 00	75767 V285)	1017	831361 QV4-MT00	334373 QVI	21835 RC5-MT02	3 he28d03.x	00749 UI-R-EB1	F290038 EST45462	8357 EST23664	904561 PM3-MT	624584 HS 2110	ription	

## ALIGNMENTS

	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION			DEFINITION	LOCUS	AQ624584/c	RESULT 1
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Homo sapiens	Homo sapiens (human)	GSS.	AQ624584.1 GI:5086976	AQ624584	sequence.	sapiens genomic clone Plate=2110 Col=11 Row=H, genomic survey	enomi	AQ624584 606 bp DNA linear GSS 16-JUN-1999		

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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                     21 IleLeuGlyGluArgTyrProIleCysCysTyr 31
                                               1 (bases 1 to 329)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Nagai,M.A., da Silva,W. Jr., Matsukuma,A., Baia,G.S., Simpson,D.H., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
     Simpson, A.J. Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                           BF904561.1 GI:12296020
                                                                                                                                                                                                                                                               BF904561 329 bp mRNA linear PM3-MT0200-211200-002-all MT0200 Homo sapiens cDNA, BF904561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clones may be purchased from Research Genetics (info@resgen.com)
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2110 row: H column: 11
Seq primer: M13 Reverse
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Meller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.,
                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Mahairas GG, Wallace JC, Hood
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle,
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
   sequence tags
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/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
1 128 c 131 g 172 t 6 others
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/db_xref="taxon:9606"
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                            134 CAGGGAAGACTCTGGCCATTCTGCTGC
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EST236647 Normalized
              Gene Index
Unpublished
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Seq primer: puc 18 forward
High quality sequence start: 2
High quality sequence stop: 329.
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Ludwig Institute for Cancer Research
Ludwig Tarchic Prudente 109, 4 an
Contact: Lee,
                                                         Rat Genome Project: Generation of a Rat EST
                                                                            Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Kerlavage, A.R. and Adams, M.D.
                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Simpson A.J.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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/db xref="caxon:9606"
/db xref="caxon:9606"
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/clone_lib="MT0200"
/note="Organ: marrow; Vector: pucl8; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196
.716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplifications."

82 c 85 g 85 t 1 others
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sp. cDNA clone
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468 bp mRNA linear EST 28-NOV-2000 EST454629 Rat Gene Index, normalized rat, Rattus norvegicus cDNA Rattus norvegicus cDNA clone RGIHM93 3' sequence, mRNA sequence.
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                                                                                                                                                                                                                                                      Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockvil
Tel: (301)-838-3529
                                                                                                                                                                                                                                                                                                                              Unpublished Other_ESTs: EST352370
                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 468)
Malek, R.L., Cho, J., Lee, Y., Karamycheva, S., Parvizi, B., Pe.
Sultana, R., Tsai, J., White, J., Quackenbush, J. and Lee, N.H.
Generation of ESTs from Normalized Rat Embryo, Bento Soare
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                           Fax: (301)-838-0208
Email: nhlee@tigr.org
This clone is available through the ATCC,
tel#703-365-2700 for further information.
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Seq primer: M13-21.
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/note="Organ: ovary; Vector: pT7T3Pac; Site_1: EcoRI;
Site_2: NotI"
a T18 c 106 g 119 t
norvegicus cDNA"
         /organism="Rattus norvegicus"
/mol_type="mRNA"
/mol_type="mRNA"
/db xref="taxon:10116"
/clone="RGIHM93"
/tissue_type="mixed tissue"
/lab_host="DH5-alpha"
/clone_lib="Rat_Gene_Index, normalized rat,
                                                                                                                                                            Location/Qualifiers
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/db_xref="taxon:10118"
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                                                                                                                                                                                                                                                                                       Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the normalized duodenum library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University of Iowa 375 Newton Road ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 547)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two appr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9Q200749 S47 bp mRNA linear EST 02-MAY-:
UI-R-EB1-clq-e-09-0-UI.sl UI-R-EB1 Rattus norvegicus cDNA clone
UI-R-EB1-clq-e-09-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                          Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 118-200, >(GAA)n#Simple_repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coordinated Laboratory
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97044477
                                                                                                                                                                                                                       Seq primer: M13 Forward
POLYA=Yes.
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a 122 c 110 g 119 t
                                                                    /organism="Rattus norvegicus"
/mol type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-EB1-clq-e-09-0-UI"
/dev_stage="adult"
/lab_host="DHIADE (Life Technologies)"
/clone_lib="VII-R-BE1"
/note="Vector: pT7T3D-Pac (Pharmacia)
                                                                                                                                                                                              location/Qualifiers
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pT7T3D-Pac (Pharmacia) with
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DB:
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                                                                                                                                                                                                    Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
Seq primer: -40UP from Gibco
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hom
1 (Dases 1 to 287)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
Mational Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AW467913.1 GI:7038019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
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/clone="IMAGE:2920325"
/tissue type="mycloid cells, 18 pooled CML cases, rearrangement positive, includes both chronic phas myeloid blast crisis"
/lab_host="DH10B"
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TAG_SEQ=TGTGGTTCAT"
130 c 119 g
                                                                                           /mol_type="huxar.
/db_xref="taxon:9606"
                                                                                                                              organism="Homo sapiens"

mol_type="mRNA"
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 LeuGlyGluArgTyrProIleCysCys 30
                                                                                                                                                                                                                                                                   Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-MT0259-
170101-011-A09&t3=2001-01-17&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 349)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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                                                                                                                                                                                                                                                                                                                                                                                                            Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shotgun sequencing of the human transcriptome with ORF expressed
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RC5-MT0259-170101-011-A09 MT0259 Homo sapiens cDNA,
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                                                                                                                                                                                                                                                       primer: puc 18 forward
                                                                                                                                                                                                             quality sequence stop: 274.
Location/Qualifiers
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               /organism="Homo sapiens"

mol_type="mtaxon:9606"

/dbv_stef="htaxon:9606"

/dev_stage="Adult"

/clone lib="MYT0259"

/note="Togan: marrow; Vector: pucl8; Site_1: Smal; Site_2:

Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="NCI_CGAP_CML1"
/note="Organ: whole blood; Vector: pCMV-SPORT6; Site_1:
SalI; Site_2: NotI; Cloned unidirectionally. Primer:
Oligo dT. Library constructed by Life Technologies."
70 q 80 t 1 others
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  Ludwig Institute for Cancer Research)
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Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.F.

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.F.

Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BQ334373 181 bp mRNA linear QV1-MT0166-131100-482-a05 MT0166 Homo sapiens cDNA,
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                                                                                                                                                                                                                                                                             This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV1&t2=QV1-MT0166-131100-482-a05&t3=2000-11-13&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                 Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                        Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                             Tel: +55-11-2704922
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence tags
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h quality sequence stop: 7.
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/note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             into
mRNA
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                                                                                                                          /dev
                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                      ocation/Qualifiers
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                                                                                                                          stage="Adult"
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91 c 96 g 73 t 1 others
                                                                                                       lib="MT0166"
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Pred. No.:
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                                                                                                                                                                                                                                                                                        Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV4-MT0050-220
600-262-c11&t3=2000-06-22&t4=1)
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Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE831361 219 bp mRN
QV4-MT0050-220600-262-c11 MT0050 Homo
BE831361
BE831361.1 GI:10263752
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Re
                                                                                                                                                                                                                                                                                                                                                                                                               Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence tags
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                                                                                                                                                                                                                                                                        primer: puc 18 forward
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                                                                                                                                                                                                                                    quality sequence stop: 219.
Location/Qualifiers
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/clone_lib="MT0050"
/note="Organ: marrow; Vector: puc18; Site_1: SmaI, Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
                                                                                                                         /mol_type="https://mol_type="https://mol.9606"
/db_xref="taxon:9606"
/dev_stage="Adult"
/dev_stage="Adult"
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48 c 44 g !
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mol_type="mRNA"
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RESULT 10
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Reams, D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult (C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White (O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald (L.M., Fitzhugh, M.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Shirley, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, B.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Husson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and
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                                                                                    Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                             Other_ESTs: THC169174
Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                  Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                           Bioinformatics
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Mammalia; Eutheria;
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1 58 c 62 g '
                                                                    Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
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US-10-045-180A-6 (1-31) x AA321199 (1-225)
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Best Local Similarity:
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                                                                                                                  The Institute for Genomic Research 9712 Medical Center Drive, Rockville,
                                                                                                                                                                                                      Other_ESTs: THC169174
Contact: Kerlavage, A
                                                                                                                                                                                                                                                                                                                         Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EST23961 Bone marrow Homo sapiens cDNA 5' end similar to defensin
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      For clone
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    mRNA sequence.

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arkerlav@tigr.org
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/db_xref="taxon:9606"
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additional sequence and expression
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AW075767/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW075767 233 bp mRNA linear EST 13-OCT-1999 xa85b06.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2573555 3' similar to gb:M26602 NEUTROPHIL DEFENSINS 1, 2 AND 3 PRECURSOR
                                                                                                                 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 226.
Location/Qualifiers
                                                                                                                                                                                                                                                            Tissue Procurement: Elisabeth Paietta, Jonathan D. Licht, M.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Literate Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University
                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 233)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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                                                                                                                                                                                                                                              Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                              Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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AW075767
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                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2573555"
tissue_type="myeloid"
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/db_xref="ATCC (inhost):122032"
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                                                                                                                                                                                                                                                                                                                                                                              Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CysHisCysArgValLeuTyrCysIlePheGlyGluHisLeuGlyGlyThrCysPheIle 21
                                                                                                                                                                                                     Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3&t2=QV3-MT0129-
111100-427-a02&t3=2000-11-11&t4=1)
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1 (bases 1 to 234)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Baia, G.S., Simpson, D.H., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soaree, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BF893374 234 bp mRNA linear QV3-MT0129-111100-427-a02 MT0129 Homo sapiens cDNA, BF893374
                                                                                                                                                                                                                                                                                                                       Tel: +55-11-2704922
Fax: +55-11-2707001
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Homo sapiens
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                                                                                                                                                quality sequence stop: 234.
Location/Qualifiers
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                     /organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
/dev stage="Adult"
/clone_lib="MT0129"
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/note="Organ: whole blood; Vector: pCMV-SPORT6;
Sall; Site 2: NotI; Cloned unidirectionally. Pr
Oligo dT. Library constructed by Life Technolo
a 49 c 55 g 67 t
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/note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2:
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1 (bases 1 to 241)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Magai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Magai,M.A., da Silva,W. Jr., Zago,M.A., Baia,G.S., Simpson,D.H., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOllveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                           This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM3&t2=PM3-MT0205-050301-004-dl0&t3=2001-03-05&t4=1)
Seq primer: puc 18 forward control of the primer control of the 
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High quality sequence stop: 241.
Location/Qualifiers
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: asimpson@ludwig.org.br
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                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2:
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                                                                                                                                                                                                                                    181200-278-H04&t3=2000-12-18&t4=1)
Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                               This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-MT0179-
                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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1 (Dases 1 to 246)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
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                                                                                                                                                                                                                                                                                                                                                                                 Tel: +55-11-2704922
Fax: +55-11-2707001
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55 c 62 g 63 t
/organism="Homo sapiens"
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/mol_type="mRNA"
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/dev_stage="Adult"
/clone_lib="MT0179"
/note="Organ: marrow; Vector: puol8; Site_1: Smal; Site_2:
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ORIGIN
Search completed: December 17, 2003, 18:25:48 Job time : 1085.85 secs
                                                                                                                                                                                US-10-045-180A-6 (1-31) x BF903426 (1-246)
                                                                                                                                                                                                                                                                                       Pred. No.:
                                                                                                                                                                                                                                                                         Score:
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                                                              126 CAGGGAAGACTCTGGCATTCTGCTGC 152
                                                                                                                   22 LeuGlyGluArgTyrProIleCysCys 30
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                                                                                                                                                                                                                                                                                                                                              Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                            0.633
80.00
55.17%
44.83%
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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-MODEL-frame+ p2.model -DEV=xlp
-Q-/cgrn2_1/USPTO_spool_p/US10045180/runat_17122003_145023_12520/app_query.fasta_1.860
-Q-/cgrn2_1/USPTO_spool_p/US10045180/runat_17122003_145023_12520/app_query.fasta_1.860
-DB=N_Geneseq_19Jun03_-QFMT=fastap -SUPFIX=ring -MINMARCH=0.1 -LCOPCL=0
-LOOPEXT=0 -UNITS=bits -STRART=1 -END=-1 -WATRIX=blosum62 -TRANS=human40 -cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE-LOCAL -OUTFWT=pco -NORM=ext -HEARSIZES=500 -MINLEN=0 -MAXLEN=200000000
-USER-US10045180 @GGN 1 1 835 @runat 17122003 145023 12520 -NCPU=6 -ICPU=3
-NO_MAAP -LARGEQÜERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMBOUT=120 -WARN_TIMBOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Listing first 45 summaries
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1: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
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7: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
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Ygapop 10.0 ,
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191
| SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.AAT: *
| SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT: *
| SIDS1/gcgdata/geneseq/geneseqn-embl/NA198.DAT: *
| SIDS1/gcgdata/geneseq/geneseqn-embl/NA198.DAT: *
| SIDS1/gcgdata/geneseq/geneseqn-embl/NA199.DAT: *
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Copyright (c) 1993 - 2003 Compugen Ltd.
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and is derived by analysis of the total score distribution.

## SUMMARIES

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X8X2222X8X cDNA sequence encoding human defensin (Def-X) protein.

Human defensin; Def-X; antimicrobial; antiparasitic; pesticide; cytostatic; anticancer; inflammation; tissue repair; endocrine regulation; corticostatic regulation; cancer; melanoma; AIDS; immune deficiency; psoriasis; ss.

Homo sapiens

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AAX26698
ID AAX2
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AC AAX2
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Human defensin; Def-X; antimicrobial; antiparasitic; pesticide; cytostatic; anticancer; inflammation; tissue repair; endocrine regulation; corticostatic regulation; cancer; melanom
                                                                                         18-JUN-1999
                                                                                                                        AAX26698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC polypeptide an be used as an antimicrobial, antiparasitic agent or CC a pesticide. The Def-X polypeptide can be used as a cytostatic CC (especially anticancer) agent, and as an agent for modulating processes CC of inflammation, tissue repair and endocrine (especially corticostatic) CC regulation. The polypeptide can be used in a composition for external CC topical use, especially in a cosmetic composition. Compositions CC containing Def-X can be used for prevention and treatment of microbial CC and parasitic infections, especially where the microbial or parasitic infections are Gram-positive or -negative bacterial infections or CC mycobacterial, fungal or spirochaete infections, or where the viral infections are associated with enveloped viruses, especially HSV and HIV. CC The compositions can used for prevention and/or treatment of cancers, CC especially melanomas, or liver cancer, prostate cancer, non-small-cell CC lung cancer or colorectal carcinoma, and for enhancing immunity, CC especially in the case of AIDS, or preventing immune deficiency, CC inflammatory processes, especially in the case of chronic inflammatory
                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
          Nucleotide sequence of human defensin (Def-X).
                                                                      AAX26696;
                                         18-JUN-1999
                                                                                                 AAX26696
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 453
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                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC The present sequence encodes human defensin (Def-X). The Def-X CC polypeptide can be used as an antimicrobial, antiparasitic agent or CC a pesticide. The Def-X polypeptide can be used as a cytostatic confinity anticancer agent, and as an agent for modulating processes CC of inflammation, tissue repair and endocrine (especially corticostatic) CC regulation. The polypeptide can be used in a composition for external CC containing Def-X can be used for prevention and treatment of microbial containing Def-X can be used for prevention and treatment of microbial CC and parasitic infections, especially where the microbial or parasitic infections are cram-positive or -negative bacterial infections or mycobacterial, fungal or spirochaete infections, or where the viral compositions can used for prevention and/or treatment of cancers, compositions can used for prevention and/or treatment of cancers, compositions can used for prevention and/or treatment of cancers, compositions can used for prevention and/or treatment of cancers, composition the case of AIDS, or preventing immune deficiency, composition the case of AIDS, or preventing immune deficiency, composition in the case of AIDS, or preventing immune deficiency.
                                                                                                                                                                                                                                                                                                                      Local
   19-MAR-1999
                                  AAV83787;
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-183266/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anticancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bougueleret L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human defensin; Def-X; antimicrobial; antiparasitic; pesticide; cytostatic; anticancer; inflammation; tissue repair; endocrine regulation; corticostatic regulation; cancer; melanoma; AIDS; immune deficiency; psoriasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-AUG-1997;
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                                                                                                                                                                                          4181
                                                                                                                            4241
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                                                                                                                                                                                                                                                                                                                  Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          defensin polypeptide Def-X - useful as antimicrobial agent, ancer agent, pesticide, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.
                                                                                                                                          IleLeuGlyGluArgTyrProIleCysCysTyr
                                                                                                                                                                                     ATCTGCCATTGCAGAGTACTATACTGCATTTTTGGAGAACATCTTGGTGGGACCTGCTTC
                                                              standard;
                                                                                                                        ATCCTTGGTGAACGCTACCCAATCTGCTGCTAC 4273
                                                                                                                                                                                                       IleCysHisCysArgValLeuTyrCysIlePheGlyGluHisLeuGlyGlyThrCysPhe 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fig 2; 56pp; French
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                              ₿₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SA.
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                                                                                                                                                                                                                                                                                                                                                                                                            1128 A; 1109
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                                                              DNA;
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                         912 G; 1252 T; 14 other;
                                                                                                                                                                                                                                                                                                                               Conservative:
                                                                                                                                                      31
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31
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(KOAD )
                                                                                         09-APR-1998;
28-MAY-1997;
                                                                                                                                                                                                                                                                                                                              Antimicrobial; fusion; acidic peptide; recombinant; microorganism;
                                                                                                                                                                                                                                                                                                                                                         Antimicrobial peptide HNP-I encoding DNA.
WPI; 1999-059844/05.
                          Hong S,
                                                                                                                                  28-MAY-1998;
                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                       guamerin; basic
                                                                                                                                                                                     WO9854336-A1
                                                                                                                                                                                                                                                                                  Homo
                                                                                                                                                                                                                                                                             sapiens
                                                 KOREA ADV INST SCI & TECHNOLOGY. SAMYANG GENEX CORP.
                       Kang MH,
                                                                                        98KR-0013372.
97KR-0021312.
                                                                                                                                98WO-KR00132.
                                                                                                                                                                                                                                                                                                                       peptide; HNP-I; ss.
                                                                                                                                                                                                              /*tag=
/note=
                                                                                                                                                                                                                                        Location/Qualifiers
                        Kim JH,
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                        Lee
                                                                                                                                                                                                            stop codons are not indicated*
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                       Lee
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New method for mass production of antimicrobial peptides - by constructing fusion genes comprising acidic and antimicrobial peptide genes and transforming host with vector containing th these

Example 6; Page 18; 52pp; English.

The invention relates to mass production of antimicrobial peptides. The combined comprises constructing a fusion gene containing a first gene cancoding a negatively charged acidic peptide having at least two cysteine cresidues, and a second gene encoding a positively charged basic antimicrobial peptide. A host microorganism is transformed with a vector containing the fusion gene and then cultured. The expressed antimicrobial peptides in recombinant microorganisms. The inhibitory effect of the expressed antimicrobial peptide upon the growth of the host microorganism is considerably reduced by fusing it to the acidic peptide. Therefore, the use of the fusion gene provides an economic, recombinant alternative of mass producing antimicrobial peptides, which overcomes the disadvantages of low-productivity and poor economy, previously encountered by recombinant and chemical methods. The present sequence represents the DNA encoding an antimicrobial peptide HNP-1. This can be used along with the acidic peptide Guamerin gene in the

Sequence 90 BP; 9 A; 27 C; 31 G; 23 T; 0 other;

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                                                            US-10-045-180A-6 (1-31) x AAV83787
                                                                              Query Match:
DB:
                                                                                               Best Local Similarity:
                                                                                                     Percent Similarity:
                                                                                                                 SCOLE
                                                                                                                         No.:
22 LeuGlyGluArgTyrProIleCysCys 30
                      CysHisCysArgValLeuTyrCysIlePheGlyGluHisLeuGlyGlyThrCysPheIle 21
                                                                            80.00
55.17%
44.83%
41.88%
                                                                                                                       0.00784
                                                            (1-90)
                                                                            Gaps:
                                                                                                              Matches:
                                                                                     Mismatches:
Indels:
                                                                                                      Conservative
                                                                            001313
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63

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Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                   The present sequence, which encodes human NP-1 (an amphiphilic peptide) is used in 2 novel methods for the recombinant prodn. of the method comprises transforming a protease deficient (PD) microbial host cell with an expression vector conty. The DNA, under the control of a regulatory sequence operable in the cost, and expressing the peptide in the transformed host. The 2nd method comprises transforming an E. coli PD K-12 cell with a vector that expresses a cleavable fusion protein, comprising at least part of a carbohydrate binding protein (CBP) and the peptide, expressing the expressing the protein to obtain the cell and cleaving the protein to obtain the peptide substantially free of CBP residues. These methods for producing and processing human NP-1 allow high levels of the peptide to accumulate in certain PD microbial host cells, despite the peptide anti-microbial potency, and efficient recovery of the full lengtide anti-microbial potency, and efficient recovery of the canalogous peptides, exhibits a broader range of activity and/or peptide may be used as an anti-parasitic, anti-fungal, anti-tumour,
                                                                                                    Sequence 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli; K-12 cell; vector; cleavable fusion protein; carbohydrate binding protein; anti-parasitic; anti-fungal; anti-tumour; anti-cancer; anti-viral; anti-microbial; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 24; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                antimicrobial, antiviral and anticancer peptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             microbial host,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anderson GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JUL-1995;
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                                                          No::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human NP-1; amphiphilic peptide; recombinant production;
protease deficient; microbial host cell; expression vector;
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                                                                                                                               or an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94US-0282030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95WO-US10219
                                                                                                                                                                                                                                                                                                                                                                                                                                                               pref.
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                                                                                                    20
                                                                                                                             anti-viral agent.
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55.17%
44.83%
41.88%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           of amphiphilic peptide in protease deficient
E. coli K-12 - useful in prodn. of
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Conservative: Mismatches: Indels:
                                         Length:
Matches:
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FXGXFFFXGXFFFXGXFXFXFXFXFXFXFXFXFXFXGXSSSSSSFFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ29363
                                 The present DNA sequence encodes an antimicrobial peptide, human alpha defensin. It is used along with a derivative of purF gene sequence that functions as a fusion partner. A DNA construct that comprises, this antimicrobial peptide encoding sequence and the entire, partial or derivative of purF gene, is used for mass production of the antimicrobial peptide in microorganisms without killing the host cells. Use of the purF gene derivative sequence, neutralises the toxicity of the antimicrobial peptides against the host microorganism. The antimicrobial peptides are
                                                                                                                                                                                          New DNA constructs useful in microorganism hosts -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        purf gene; glutamine pyrophosphoribosyl pyropho
purf derivative; fusion partner; antimicrobial
mass production; cleavage site; hydroxylamine;
neutralise; toxicity; pharmaceutical industry;
                                                                                                                                                                 Claim 1;
                                                                                                                                                                                                                                                                                                                                    09-JUN-1998;
14-MAY-1999;
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                                                                                                                                                                                                                                     P-PSDB;
                                                                                                                                                                                                                                                                              Kim JH,
                                                                                                                                                                                                                                                                                                                                                                             08-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                        16-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antimicrobial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ29363 standard;
                                                                                                                                                                                                                                                                                                        (SAMY-) SAMYANG GENEX CORP.
                                                                                                                                                                                                                                                  2000-097542/08.
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                        commercially in the pharmaceutical and food industries
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                                                                                                                                                                                                                                     AAY44323.
                                                                                                                                                              Fig 1; 67pp;
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                                                                                                                                                                                                                                                                             Kang MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGGGTCGTCTGTGGGCATTCTGTTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide,
                                                                                                                                                                                                                                                                                                                                   98KR-0022117
99KR-0017920
                                                                                                                                                                                                                                                                                                                                                                             99WO-KR00282
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "Human alpha defensin peptide"
/note= "Antimicrobial peptide used in DNA construct"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                              Lee
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                                                                                                                                                                 English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human alpha defensin
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                                                                                                                                                                                                                                                                             HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ribosyl pyrophosphate amidotransferase;
antimicrobial peptide; alpha defensin;
pydroxylamine; CNBF; DNA construct;
ical industry; food industry; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                        production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30
                                                                                                                                                                                                                                                                             Lee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoding DNA.
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fi
                                                                                                                                                                                                                                                                           Hong
                                                                                                                                                                                                       antimicrobial peptides
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                                                                                                                                                                                                                                                                             ss,
                                                                                                                                                                                                                                                                             Lee
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Percent Similarity: Best Local Similarity:

80.00 55.17% 44.83%

Length: Matches: Conservative:

13

0.00998

Pred. No.:

Sequence 110

B₽;

14 A; 31 C;

37

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28 T; 0 other;

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RESULT 7
ABL60444
ID ABL6
 Score:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
                                                                                 The invention relates to a genetic component which mass-produces peptide antibiotics effectively from microorganisms. The genetic component consists of a first gene sequence which codes for the whole or partial purf gene or its derivative, and a second gene sequence which codes peptide antibiotics. The mass-production method of peptide antibiotics comprises the steps of; constructing an expression vector including the genetic component, transforming a bacterial host cell with the vector, culturing the transformed cell to express the genetic component, and recovering the peptide antibiotics. The expression vector is selected from the group consisting of pGNN2, pGNN3, pGNN3 and pGNN5, and it has a high copy number of origin, strong transcription promoter and structural gene. The sequences given in records ABL60400-ABL60464 represent DNA sequences of the invention.
                                                                                                                                                                                                                                                                      Disclosure; Page 16; 56pp; Korean.
                                                                                                                                                                                                                                                                                                         Gene expression system useful for mass-production of peptide
                                                                                                                                                                                                                                                                                                                                     P-PSDB;
                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-301977/34.
                                                                                                                                                                                                                                                                                                                                                                                                                             08-JUN-2001; 2001KR-0031889
                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JUN-2001; 2001KR-0031889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                       (SAMY-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KR2001098973-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA fragment of the invention HNP-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABL60444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABL60444 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression; peptide antibiotic; purf gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                           Kang MH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCTACTGCCGTATCCCGGCGTGCATCGCGGGTGAGCGTCGTTACGGTACCTGCATCTAC 73
                                                                                                                                                                                                                                                                                                and
                                                              ВP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                               vectors
                                                              14 A; 31 C;
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/note= "no start codon
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAI88805
                                                                               The invention relates to human polymucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published not semisores
                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 8865; 1399pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                        Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2000;
18-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-FEB-2001; 2001WO-US04927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAI88805 standard;
                                                                                                                                                                                                                                                                                                                                                            P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-514838/56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200164835-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human polynucleotide SEQ ID NO 8865
                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-)
                                                                            inflammation.
                      ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                          Liu C,
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2000US-0577409.
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Alignment Scores: Pred. No.:

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Length: Matches:

159

Sequence 159

49 A; 34 C;

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Best Local S:
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Best Local Similarity:
(I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonuclectides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adhesion molecules and their receptors, contral nervous system (CNS) and peripheral nervous and non-nervous system
                                                                                                                                                                                                                                                                                                     trigger
cancers
                                                                                                                                                                                          oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base.
                                                                                                                                                                                                                          The present invention describes low adenosine (A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection;
                                                                                                                                                                                                                                                               Disclosure; Page 218; 1592pp; English
                                                                                                                                                                                                                                                                                                                Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating
                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-679539/66
                                                                                                                                                                                                                                                                                                                                                                                                           Мусе JW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Low adenosine antisense oligonucleotide; phosphorothicate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-MAR-2000; 2000WO-US08020
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                                                                                                                                                                                                                                                                                                     and respiratory obstructions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CysHisCysArgValLeuTyrCysIlePheGlyGluHisLeuGlyGlyThrCysPheIle 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phosphorothicate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; antiinflammatory; antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthmatics; and disease; ischaemic condition; pulmonary vasoconstriction; asthmatics; line disease; ischaemic condition; pulmonary vasoconstriction; asthmatics; line disease; line disease
                                                                                                                                                                                                                                                            03-AUG-1998;
                                                                                                                                                                                                                                                                                                                   03-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200009525-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; adenosine receptor; low adenosine antisense oligonucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human adenosine receptor related polynucleotide SEQ ID NO:2478.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA34789 standard; DNA; 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptors, CNS and peripheral nervous and non-nervous system peptide
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New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension,

WPI; 2000-205971/18.

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-045-180A-6 (1-31) x AAA34789 (1-464)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONs reduces side effects. The A-containing ONs break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
                                                                                                                                                EP1033401-A2
                                                                                                                                                                                                                                                              Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
                                              21~FEB-2000; 2000EP-0200610.
                                                                                                                                                                                                                                                                                                                       Human secreted protein 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC04468 standard; cDNA; 478 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 464 BP; 110 A; 128 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 sequences are also called SEQ ID NO:1 to 185 but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to AAA3392) are specifically claimed ONs from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence listing.
                                                                                                 06-SEP-2000
                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                          06-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiaethmatic, cytostatic and analgesic activities. The compositions are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 612; 1343pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful for the treatment of diseases associated with inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bronchitis, emphysema, respiratory distress syndrome, ischemia or
                                                                                                                                                                                                                                          therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      345 CAGGGAAGACTCTGGGCATTCTGCTGC 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuGlyGluArgTyrProlleCysCys 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CysHisCysArgValLeuTyrCysIlePheGlyGluHisLeuGlyGlyThrCysPheIle 21
                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                       chromosome mapping; ss
99US-0122487
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Conservative:
Mismatches:
Indels:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is one of a large number of 5' ESTs derived from CC mkNAs encoding secreted proteins. No ORF has yet been conclusively CC identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) CC for the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design cexpression and secretion vectors.
                           US5066792-A.
                                                                      polyA_signal
                                                                                                                      CDS
                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                        CML; Philadelphia chromosome; myeloid-related sequence;
                                                                                                                                                                                                                                        Chronic myelogenous leukaemia-derived mrs cDNA.
                                                                                                                                                                                                                                                                           25-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                chromosome 8; ss.
                                                                                                                                                                                                                                                                                                                                     AAQ14908 standard; cDNA; 498 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                           22 LeuGlyGluArgTyrProIleCysCys 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCTATTGCAGAATACCAGCGTGCATTGCAGGAGAACGTCGCTATGGAACCTGCATCTAC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP;
                                                                                                                                                                                                                                                                          (first
                                                                                  16..378
/*tag= a
/note= "see comments"
                                                                       479..484
                                                                                                                                  Location/Qualifiers
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Mismatches:
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28-SEP-1984;
04-SEP-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The precise position of the CDS is unsure due to the 13 unidentified nucleotides at the 5' end of the sequence. The most likely position for initiation of translation occurs at nucleotide 94 and the open reading frame following this point is claimed. The first 18 codons of the claimed ORF (excluding the ATG) encode a sequence of amino acids that resembles other leader sequences and their cleavage sites. The mrs sequence was isolated as clone C-AJ (ATGC 39868) from a cDNA library constructed from total RNA from a patient suffering from chronic phase, Ph'-positive CML. The mrs is localised to human chromosome 8, specifically to bands 8q21.1-23.
 22-AUG-2002
                           WO200264832-A1
                                                                                                                                            human;
                                                                                                                                                                                 Human defensin 1 coding sequence.
                                                                                                                                                                                                              11-NOV-2002
                                                                                                                                                                                                                                         ABQ80601;
                                                                                                                                                                                                                                                                 ABQ80601 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene probe for chronic myelogenous leukaemia - distinguishing myeloblastic crisis from lymphol
                                                                                                                                                         Antiallergic;
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                                                                                                                                                      allergic disease; allergy; defensin 1; atopic dermatitis;
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84US-0655942.
87US-0094099.
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                                                            Location/Qualifiers
94..378
/*tag= a
                                                 /*tag= a
/product= "Human defensin
                                                                                                                                                                                                                                                                DNA; 498
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80.00
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Conservative:
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from lymphoblastic crisis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            other;
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RESULT 14
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Best Local Similarity:
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                                                                   06-SEP-2000.
                                                                                                                  Homo
                                                                                                                                        gene
                                                                                                                                                                           Human secreted protein 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 498 BP; 118 A; 134 C; 122 G; 111 T;
                      26-FEB-1999;
                                           21-FEB-2000;
                                                                                          BP1033401-A2
                                                                                                                                                     Human; 5' EST;
                                                                                                                                                                                                    06-OCT-2000
                                                                                                                                                                                                                            AAC00098;
                                                                                                                                                                                                                                                 AAC00098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diseases. The method comprises: (a) determining the expression level of defensin 1 gene in the biological sample from a patient; and (b) comparing the expression level with that in the sample of a healthy individual. The method is for examining allergic diseases particularly atopic dermatitis and its diagnosis, which is also applicable in screening candidate compounds for remedies. The present sequence is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Examining allergic diseases by changes in expression levels of defensini gene in peripheral blood monocytes as indication, also applicable in screening compounds for treating of allergic diseases e.g. atopic dermatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 45-46; 57pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sugita Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-FEB-2001; 2001JP-0036362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-FEB-2002; 2002WO-JP01193
(GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a method for examining allergic diseases. The method comprises: (a) determining the expression l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NIGE-) JAPAN
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                                                                                                                 sapiens.
                                                                                                                                       therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence for human defensin 1.
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                                                                                                                                                                                                                                                                                                                                                            CysHisCysArgValLeuTyrCysIlePheGlyGluHisLeuGlyGlyThrCysPheIle
                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                CAGGGAAGACTCTGGGCATTCTGCTGC 375
                                                                                                                                                                                                                                                                                                                     LeuGlyGluArgTyrProIleCysCys 30
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                                            2000EP-0200610
                                                                                                                                                                                                  (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GEN AGENCY NATION
                                                                                                                                       chromosome mapping;
                     99US-0122487
                                                                                                                                                  expressed sequence tag; secreted protein; cDNA isolation;
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80.00
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                  498
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RESULT 15
ABN59722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain vectors.
                                                                                                                                                                                                                                                                                                      Human; antianaemic; vulnerary; antiinflammatory; immunomodulator; antiinfertility; cerebroprotective; cytostatic; rheumatic; gene t neuroprotective; antiparkinsonian; protein therapy; EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity:
                                                 11-SEP-2000; 2000US-0659671
                                                                                                10-SEP-2001; 2001WO-US26015
                                                                                                                                             21-MAR-2002
                                                                                                                                                                                            WO200222660-A2
                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                     expressed sequence tag; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                            Novel human
(HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABN59722 standard; cDNA; 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 509 BP; 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CysHisCysArgValLeuTyrCysIlePheGlyGluHisLeuGlyGlyThrCysPheIle 21
                                                                                                                                                                                                                                                                                                                                                                                                       coding sequence SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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Search completed: December 17, 2003, 15:06:05
Job time : 118.25 secs

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Query Match:
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                                                                                                                                                                                                                                                                                            (BSTs). They can be used to stimulate cell growth, to regulate haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. Parkinson's disease. The present sequence is a coding sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang YT,
Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 133; 509pp; English.
                                                                                                                                                                                                                                                           Sequence 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  An isolated polynucleotide for treating diseases associated with encoded polypeptide such as cancer and multiple sclerosis -
                                                                                                                                                                                                                                                                                       invention.
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                                                         292
352 CAGGGAAGACTCTGGGCATTCTGCTGC
                          22 LeuGlyGluArgTyrProIleCysCys
                                                                                     N
                                                   TGCTATTGCAGAATACCAGCGTGCATTGCAGGAGAACGTCGCTATGGAACCTGCATCTAC 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu '
                                                                            CysHisCysArgValLeuTyrCysIlePheGlyGluHisLeuGlyGlyThrCysPheIle 21
                                                                                                                                                                                                                                                           BP;
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Matches:
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Indels:
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Command line parameters:

-MODEL-frame+ p2n.model -DEV=xlp
-MODEL-frame+ p2n.model -DEV=xlp
-MODEL-frame+ p2n.model -DEV=xlp
-MODEL-frame+ p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_Spool_p/US10045180/runat_17122003_145026_12635/app_query.fasta_1.860
-DB=Published_Applications_NA_-QFWT=fastap_-SUFFIX=rnpb -MINMATCH=0.1
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=bib.osum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_WAX=100
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_WAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=pto -NORM=ext -HEAPSTZB=500 -MINLEN=0
-MAXIEN=2000000000 -USER=US10045180 @CGN 1 1 174 @runat 17122003 145026 12635
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -
-LOOPECD_DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGĀPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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| Cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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| Cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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963.776 Million cell updates/sec
        Description
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                                                                                                                                                                                                                                                Sequence 2, Application US/10013770
Publication No. US20020115151A1
GENERAL INFORMATION:
APPLICANT: GENSET SA
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                      NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
CORRESSEE: Knobbe, Martens, Olson & Bear
STREET: 550 West C Street
CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                        TITLE OF INVENTION: HUMAN DEFENSIN DEF-X GENE AND DNAC COMPOSITION CONTAINING SAME AND DITTHERAPEUTIC APPLICATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/10/013,770
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ALIGNMENTS

DIAGNOSTIC AND

Version

#1.30 (EPO)

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US-09-918-95-187-223
US-09-816-828-16
US-09-816-828-16
US-09-816-828-16
US-09-816-828-16
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US-09-918-92-941-1047
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US-10-127-632-106466
US-09-918-95-1878
US-10-027-632-106466
US-10-027-632-106466
US-10-027-632-2770
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US-10-027-632-25143
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US-10-013-770-1
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Sequence 1, Appli
Sequence 1, Appli
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Sequence 19070, A
Sequence 19070, A
Sequence 16, Appl
Sequence 16, Appl
Sequence 78, Appl
Sequence 1047, Ap
Sequence 1048, Appli
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                                                                        Alignment Scores:
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                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1997-08-29
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/045,180A
CURRENT FILING DATE: 2001-10-18
PRIOR APPLICATION NUMBER: US 09/486,580
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: PCT/FR98/01864
PRIOR FILING DATE: 1998-08-28
PRIOR APPLICATION NUMBER: FR 97/10823
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bougueleret, Lydie
APPLICANT: Chumakov, 11ya
APPLICANT: Chumakov, 11ya
TITLE OF INVENTION: Human Defensin Polypeptide Def-X, Genomic DNA and cDNA, Compositi
TITLE OF INVENTION: Containing Them and Applications to Diagnosis and to Therapeutic
FILE REFERENCE: GEN-100D1
                                                                                                      FEATURE:
NAME/KEY: CDS
LOCATION: (52)..(336)
CHIER IMPORMATION: Def-X coding sequence
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REGISTRATION NUMBER: 40,637
REFERENCE/DOCKET NUMBER: GENSET.064C1
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 453 BASE PAIRS
                                                                                                                                                                                                 LENGTH: 453
TYPE: DNA
ORGANISM: Homo sapiens
                                                        No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 10-Dec-2001
PRIOR APPLICATION DATA:
APPLICATION UNMBE: 09/486,580
FILING DATE: «Unknown»
ATTORNBY/AGENT INFORMATION:
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Query Match:
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COMPOSITION CONTAINING SAME AND DIAGNOSTIC AND
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NAME: Hart, Daniel
REGISTRATION NUMBER: 40,637
REFERENCE/DOCKET NUMBER: GENSET.064C1
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/013,770
FILING DATE: 10-Dec-2001
PRIOR APPLICATION DATA:
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ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 550 West C Street
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 4415 BASE PAIRS
TYPE: NUCLECTIDE
STRANDEDNESS: DOUBLE
                                                                                                                                                                                                                       FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: LINEAR MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                      FEATURE:
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STATE: California
                 NAME/KEY:
LOCATION:
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3406..3408
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3394..3577
                 polyadenylation site 4374..4379
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RESULT 4
US-10-045-180A-1
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
                                                                                                                                                                                                              PEATURE:
NAME/KEY: misc feature
LOCATION: (143)...(143)
OTHER INFORMATION: n = a
FEATURE:
NAME/KEY: misc feature
LOCATION: (670)...(670)
OTHER INFORMATION: n = a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bougueleret, Lydie
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Human Defensin Polypeptide Def-X, Genomic DNA and cDNA, Compositi
TITLE OF INVENTION: Containing Them and Applications to Diagnosis and to Therapeutic
TILE REPERENCE: CEN-100D1
CURRENT FILING DATE: 2001-10-18
CURRENT FILING DATE: 2001-10-18
PRIOR APPLICATION NUMBER: US 09/486,580
PRIOR APPLICATION NUMBER: PCT/FF98/01864
PRIOR APPLICATION NUMBER: PCT/FF98/01864
PRIOR FILING DATE: 2000-02-25
PRIOR FILING DATE: 1998-08-28
PRIOR FILING DATE: 1998-08-28
PRIOR FILING DATE: 1998-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: FR 97/10823 PRIOR FILING DATE: 1997-08-29
                                                                    FEATURE:
NAME/KEY: misc feature
LOCATION: (1111)...(1111)
OTHER INFORMATION: n = a
                                                                                                                                             FEATURE:
NAME/KEY: misc_feature
LOCATION: (970)...(970)
OTHER_INFORMATION: n =
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LOCATION: (85)..(85)
OTHER INFORMATION: n =
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NAME/KEY: misc_feature
LOCATION: (1)...(4415)
OTHER_INFORMATION: Def-X
OTHER INFORMATION: n = a FEATURE.
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                           NAME/KEY: misc_feature
LOCATION: (1150)..(115
                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH:
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NAME/KEY: CAAT signal LOCATION: (1711)..(17: OTHER INFORMATION:
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NAME/KEY: TATA signal
LOCATION: (1758)..(1767)
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LOCATION: (1875)..(1880)
OTHER INFORMATION: splice
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OTHER INFORMATION: n = a
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LOCATION: (1780)..(178
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LOCATION: (3391)...(3393)
OTHER INFORMATION: splice
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LOCATION: (2367)..(2367)
OTHER INFORMATION: n = a,
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LOCATION: (2191)..(2191)
OTHER INFORMATION: n = a
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NAME/KEY: misc_feature
LOCATION: (2186)...(2186)
OTHER INFORMATION: n = a,
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LOCATION: (2155)..(2335)
OTHER INFORMATION: Alu insertion
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                  OTHER INFORMATION: n = a FEATURF:
                                                                                    LOCATION: (3578)..(3583)
OTHER INFORMATION: splice
                                                                                                       NAME/KEY: misc feature LOCATION: (3578)..(358
                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (3406)...(3408)
OTHER INFORMATION: Translation initiation codon (ATG)
                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (3394)..(3577)
OTHER INFORMATION: Exon
                                                                                                                                                                                                                                                                                                                                   LOCATION: (2710)..(2780)
OTHER INFORMATION: L1 fragment
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LOCATION: (2710)..(278
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LOCATION: (2117)..(211
                                             NAME/KEY: misc feature LOCATION: (4123)..(412)
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misc_feature
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US-09-918-995-18198/c
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DB:
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Best Local Similarity:
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                                                           US-10-045-180A-6 (1-31) x US-09-918-995-18198 (1-337)
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                                                                                                                            Best Local Similarity:
                                                                                                                                             Percent Similarity:
                                                                                                                                                            Score:
                                                                                                                                                                             Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18198, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 18198
LENGTH: 337
                                                                                                                                                                                                                                                     NAME/KEY: misc feature LOCATION: (1)...(337)
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LOCATION: (4164)..(4379)
OTHER_INFORMATION: Exon
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LOCATION: (4274)..(4276)
OTHER INFORMATION: Translation termination codon (TAA)
                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (4161)..(4163)
OTHER INFORMATION: splic
                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: polyA_signal
LOCATION: (4374)..(437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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198 TGCTATTGCÁGAATACCAGCGTGCÁTTGCAGGAGÁACGTCGCTATGGAACCTGCATCTAC 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCTGCCATTGCAGAGTACTATACTGCATTTTTGGAGAACATCTTGGTGGGACCTGCTTC
                      CysHisCysArgValLeuTyrCysIlePheGlyGluHisLeuGlyGlyThrCysPheIle 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IleLeuGlyGluArgTyrProIleCysCysTyr 31
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Matches:
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Matches:
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APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBT
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 19070
                                                                                                                                                                                                                                GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

FITTLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OB:

TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES

FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOPTWARE: FARSEQ for Windows Version 3.0

SEQ ID NO 18323

TENERAL INFORMATION:
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Best Local Similarity:
Query Match:
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US-09-918-995-19070
US-10-045-180A-6 (1-31) x US-09-918-995-18323 (1-353)
                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                 US-09-918-995-18323
                                                  Query Match:
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Publication No. US20030073623A1
GENERAL INFORMATION:
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Publication No. US20030073623A1
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TYPB: DNA
                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                    TYPE: DNA
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Matches:
Conservative:
Mismatches:
Indels:
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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GENERAL INFORMATION:
APPLICANT: Faris, Mary
APPLICANT: Pearson, Cecelia I.
APPLICANT: Pearson, Cecelia I.
TITLE OF INVENTION: GENES EXPRESSED IN PROSTATE CANCER
FILE REFERENCE: PA-0027-1 US
CURRENT APPLICATION UNMBER: US/10/252,157
CURRENT FILLING DATE: 2002-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 223, A Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 223
                                                                                                                                                                                                                                                                                                             Sequence 16, Application US/09816828 Patent No. US20020150898A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/295,048
PRIOR FILING DATE: 2001-05-31
NUMBER OF SEQ ID NOS: 501
SOFTWARE. DEDI. DOS: 501
                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20020150898A1el Nucleic
TITLE OF INVENTION: Polypeptides
FILE REFERENCE '791CIP2E
CURRENT APPLICATION NUMBER: US/09/816,828
CURRENT FILING DATE: 2001-03-22
                                                                                                                                                                                                                            APPLICANT:
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No.
                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                             ENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    340 TGCTATTGCAGAATACCAGCGTGCATTGCAGGAGAACGTCGCTATGGAACCTGCATCTAC 399
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Zhao, Qing A.
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                                                                                                                                                                                                                   Goodrich, N.
                                                                                                                                                      Ren, Feiyan
Xue, Aidong J.
Ma, Yunqing
Wang, Zhiwei
                                                                                                  Zhang, Jie
Wang, Jian-Rui
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b. US20030190640A1
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                                                                       Acids and
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; TYPE: DNA; Homo sapiens; CRGANISM: Homo sapiens; FRATURE; NAME/KEY: CDS; IOCATION: (151)..(522)
US-09-816-828-16
                                                                                                                                       PRIOR APPLICATION NUMBER: 09/552,929
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 18
SOPTWARE: pt_FL_genes Version 2.0
SEQ ID NO 16
LENGTH: 726
TYPE: DNA
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Best Local Similarity:
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             Alignment Scores:
Pred. No.:
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                                                             US-09-816-828-16
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SOFTWARE: pt FL_genes Version 2.0
SEQ ID NO 16
LENGTH: 726
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                                                                                                                                                                                                                                                   APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20020150898A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 791CIP2E
CURRENT PPLICATION NUMBER: US/09/816,828
CURRENT FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR FILING DATE: 2001-01-26
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APPLICANT:
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PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/552,929
PRIOR FILING DATE: 2000-04-18
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                                                                            NAME/KEY: CDS
LOCATION: (151)..(522)
                                                                                                                        ORGANISM: Homo sapiens
                                                                                                            FEATURE:
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Zhao, Qing A.
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Ma, Yunging
Wang, Zhiwei
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Wang, Jian-Rui
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Asundi, Vinod
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1054 TGCTATTGCAGAATACCAGCGTGCATTGCAGGAGAACGTCGCTATGGAACCTGCATCTAC 1113
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                                                                                                                                                                                                                                                                               2 CysHisCysArgValLeuTyrCysllePheGlyGluHisLeuGlyGlyThrCysPhelle 21
                                                                                                                                                                                                                                                                                                                           100 TGCTATTGCAGAATACCAGCGTGCATTGCAGAGAACGTCGCTATGGAAACCTGCATTAC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ## SAPPLICANT: Tang, Y. Tom
## APPLICANT: Tang, P. Tom
## APPLICANT: Asundi, Vinod
## APPLICANT: Asundi, Vinod
## APPLICANT: Zhao, Qing A.
## APPLICANT: Zhao, Qing A.
## APPLICANT: Zhang, Jie
## APPLICANT: Asundi, Jiang J.
## APPLICANT: Asundi, Jiang J.
## APPLICANT: Drmanac, Raddje T.
## APPLICANT: Polypeptides
## APPLICANT: POLYPEPtides
## TITLE OF INVENTION: NO. Polypeptides
## SOFTWARE: Dr. Fi_genes Version 2.0
## SOFTWARE: Dr. Fi_genes Version 2.0
## ELENGTH: 1348
## TITLE OF INVENTION: NO. 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 78, Application US/10125237
Publication No. US20030022329A1
GENERAL INFORMATION:
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Percent Similarity: 55.17%
Best Local Similarity: 44.83%
Query Match: 41.88%
DB: 10
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ORGANISM: Homo sapiens
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US-10-125-237-78
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CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT APPLICATION NUMBER: US/09/736,457
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSEQ for Windows Version 3.0
                                                          APPLICANT: Zhou, Jungaluan APPLICANT: Zhou, Jungaluan APPLICANT: Zhou, Jungah APPLICANT: Ren, Feliyan APPLICANT: Ren, Feliyan APPLICANT: Zhao, Qing A. APPLICANT: Zhao, Qing A. APPLICANT: Zhang, Jie APPLICANT: Zhang, Jie APPLICANT: Wehrman, Tom APPLICANT: Wehrman, Tom APPLICANT: Wehrman, Tom APPLICANT: Wentwork: Radoje T. TITLE OF INVENTION: Delypeptides TITLE OF INVENTION: Polypeptides FILE REFERENCE: 791CTPZA CURRENT APPLICATION NUMBER: 2002-2.5 PRIOR FILING DATE: 2000-03-2.5 PRIOR FILING DATE: 2000-03-2.5 PRIOR FILING DATE: 2000-04-18 PRIOR FILING DATE: 2000-04-18 SOFTWARE: Pt_Legenes Version 2.0 SEQID NO 3: 500 DATE: 2000-04-18
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patent No. US20020168637A1
; GENERAL INFORMATION:
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Bangur, Chaitanya S.
Lodes, Michael A.
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Vedvick, Tom
Carter, Darrick
Retter, Marc
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                    APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
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US-10-105-891-78
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GENERAL INFORMATION:
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22 LeuglyGluArgTyrProlleCysCys 30

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APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Retranshe, Yoshihiro
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary R.
APPLICANT: Panger, Gary R.
APPLICANT: Panger, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Wordabb, Andria
ITILE OF INVENTION: CONFOSITIONS AND METHODS FOR THE THERAPY
ITILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 21012.478C17
CURRENT APPLICATION NUMBER: US/09/902,941
CURRENT FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 2002
SOFTWARE: FastSEQ for Windows Version 4.0
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; DCGATTON: 183, 271, 287, 292, 294, 343

; CTHER INFORMATION: n = A,T,C or G

US-09-902-941-1047
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                                                                        NAME/KEY: misc feature
LOCATION: (1)...(412)
OTHER INFORMATION: n = A,T,C or G
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74.00
51.72%
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ORGANISM: Homo sapiens
                TYPE: DNA
ORGANISM: Homo sapien
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US-09-736-457-1047
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LENGTH: 412
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| 1954 TGCTATTGCCGAACCGGCGTTGTGCTACCCGTGAGTCCCTCCGGGGGGTGTGTGAAATC 195
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APPLICANT: Fanger, Gary
APPLICANT: Wang, Aijun
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Switzer, Anne
APPLICANT: Clapper, Jonathan
TITLE OF INVENTION: CMCOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: CMCOSITIONS (SOCIETIONS AND METHODS FOR THE THERAPY AND
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194 AGIGGCCGCCINTACAGACTCTGCTGT 168
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                                                                                                                                                                                                                                   Sequence 1047, Application US/09849626; Publication No. US20020197669A1; PENBAL INFORMATION: APPLICANT: Bangur, Chaitanya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | NAME/KRY: misc_feature
| LOCATION: (1)...(412)
| CHER INFORMATION: n = A,T,C or G
| 195-09-845-626-1047
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US-09-849-626-1047/c
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1047, PP 1047, Ap 1047, Ap 4, Appli 1, Appli 43, Appl 43, Appl

Perfect score:

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Sequence 1198, Ar
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| Patent No. 6329340
| GENERAL INPOWENTION:
| APPLICANT: GENERATION:
| TITLE OF INVENTION: HUMAN DEFENSIN DEF-X GENE AND DNAC TITLE OF INVENTION: COMPOSITION CONTAINING SAME AND DIAGNOSTIC AND TITLE OF INVENTION: THERAPEUTIC APPLICATIONS
| NUMBER OF SEQUENCES: 6 CORRESPONDENCE ADDRESSER: Knobbe, Martens, Olson & Bear STREET: 550 West C Street
| STREET: 550 West C Street
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/486,580A
FILING DATE: FEBRUARY 25, 2000
ATTORNEY/AGENT INFORMATION:
NAME: Hart, Daniel
REGISTRATION NUMBER: 40,637
                                                                                                                                             PCT-US95-10219-50
PCT-US95-10219-62
US-09-702-705-1047
US-09-736-457-1047
US-08-158-189-4
US-09-450-972-6
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US-08-486-013-43
US-08-482-279-43
US-08-342-228-43
US-09-397-386-43
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US-08-482-279-52
US-08-342-268-52
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US-08-482-279-46
US-08-342-268-46
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US-08-282-030-62
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US-08-482-279-47
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US-09-397-386-52
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: C
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 453 BASE PAIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: DOUBLE
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STATE: California
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\begin{array}{c} \mathbf{4466} \\ \mathbf{4400} \\ \mathbf{600} \\ \mathbf{0000} \\ 
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-O=/cgn2_1/USPTO spool p/US10045180/runat_17122003_145024_12553/app_query.fasta_1.860
-O=/cgn2_1/USPTO spool p/US10045180/runat_17122003_145024_12553/app_query.fasta_1.860
-O=/cgn2_1/USPTO spool p/US100451800/cdi
-LOOPEXT=0 -UNITS=bits -STRAT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-USFNT=20000000000
-USFNT=pco -NOFM=ext -HEAPSIZE=s00 -MININENE0 -MAXLEN=200000000
-USFNT=910045180 @CGN 1 1193 @runat 17122003 145024 12553 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WALT -DSPBLOKE=100 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 1, Appl:
                                                                                                                                                                                                                                                                                                           (without alignments)
441.383 Million cell updates/sec
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Sequence 44,
Sequence 45,
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Sequence 44,
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                                                                                                                                                                                                                                                                   December 17, 2003, 14:50:33; Search time 31 Seconds
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
                                           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                            OM protein - nucleic search, using frame plus p2n model
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US-09-486-580A-1
US-09-230-180-27
US-08-282-030-43
US-08-282-030-44
US-08-282-030-45
PCT-US95-10219-43
PCT-US95-10219-45
US-08-282-030-61
US-08-282-030-61
US-08-0-282-030-61
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1 ICHCRVLYCIFGEHLGGTCFILGERYPICCY 31
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09486580A
Patent No. 6329340
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: HUMAN DEFENSIN DEF-X GENE AND DNAC
TITLE OF INVENTION: THERAPEUTIC APPLICATIONS
TITLE OF INVENTION: THERAPEUTIC APPLICATIONS
OWNER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/486,580A
FILING DATE: FEBRUARY 25, 2000
ATTORNEY/AGENT INFORMATION:
NAME: Hart, Daniel
REGISTRATION NUMBER: 40,637
REFERENCE/DOCKET NUMBER: GENSET.064C1
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4415 BASE PAIRS
TYPE: NUCLEAGINE
                                                                            453
31
0
0
                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                               Gaps:
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STRANDEDNESS: DOUBLE
TOPOLOGY: LINEAR
MOLECULE TYPE: DNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                            3.5e-19
191.00
100.00%
100.00%
             ; ORGANISM: Homo sapiens
US-09-486-580A-2
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LOCATION: 1836..1874
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LOCATION: 3394..3577
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4161..4380
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3406..3408
                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
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ORIGINAL SOURCE:
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NAME/KEY:
LOCATION:
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FEATURE:
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4181 ATCTGCCATTGCAGAGTACTATACTGCATTTTTTGGAGAACATCTTGGTGGGACCTGCTTC 4240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: DNA sequence deduced from HNP-I peptide sequence; OTHER INFORMATION: based on codon usage of E. coli US-09-230-180-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kang, Min Hyung
APPLICANT: Kang, Min Jeong Hyun
APPLICANT: Kim, Jeong Hyun
APPLICANT: Hoe, Pun-Soo
APPLICANT: Beerng-Suh
APPLICANT: Samyang Genex Corporation
APPLICANT: Samyang Genex Corporation
APPLICANT: Samyang Genex Corporation
APPLICANT: Samyang Genex Corporation
APPLICANT: Korea Advanced Institute of Science and Technology
TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE
TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE
FILE REPREBRICATION NUMBER: PSU/09/230,180
CURRENT FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: PCT/KR98/00132
PRIOR APPLICATION NUMBER: KR 13372/1998
PRIOR PILING DATE: 1998-04-09
PRIOR PILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 36
SOFTAMER: FastSEQ for Windows Version 3.0
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Matches:
Conservative:
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 27, Application US/09230180; Patent No. 6183992; GENERAL INFORMATION:
                                                        polyadenylation site 4374..4379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
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80.00
55.17%
44.83%
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100.00%
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Lee, Jae Hyun
  stop CDS
4276..4278
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Best Local Similarity:
Query Match:
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NAME/KEY:
LOCATION:
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COCATION:
US-09-486-580A-1
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LENGTH: 90
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                                   us-08-282-030-43

Sequence 43, Application US/08282030

Patent No. 5589364

GENERAL INFORMATION:

APPLICANT: Pierce, James C.

APPLICANT: Anderson, Mark G.

APPLICANT: Anderson, Mark G.

APPLICANT: Anderson, Mark G.

TITLE OF INVENTION: Recombinant Production of Biologically

TITLE OF INVENTION: Active Peptides and Proteins

NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & STREET: 1300 I Street, N.W.

CITY: Washington

STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Patentln Release #1.0, Version #1.25
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/282,030
FILING DATE: 29-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REGISTRATION NUMBER: 32,984
REGISTRATION NUMBER: 32,984
REGISTRATION NUMBER: 05387.0001-00000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-045-180A-6 (1-31) x US-08-282-030-43 (1-108)
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                  22 LeuGlyGluArgTyrProIleCysCys 30
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Patent No. 589364
GENERAL INFORMATION:
APPLICANT: Williams, Jon I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.00073
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55.17%
44.83%
41.88%
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                             D.C.
USA
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                                                                                              RESULT 4
US-08-282-030-43
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                                                                                   APPLICANT: Kari, Prasad
TITLE OF INVENTION: Recombinant Production of Biologically
TITLE OF INVENTION: Recombinant Production of Biologically
TITLE OF INVENTION: 62
NUMBER OF SEQUENCES: 62
ADDRESSE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSE: Pinnegan, Henderson, Farabow, Garrett &
ADDRESSE: ADDRESSE: CONNECT OF SETTING OF STREET ADDRESSE: ADDRESSE: DATE: D.C.
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| Patent No. 5589364 |
| GENERAL INFORMATION: |
| APPLICANT: Williams, Jon I. |
| APPLICANT: Anderson, Mark G. |
| APPLICANT: Anderson, Mark G. |
| APPLICANT: Anderson, Mark G. |
| TILLE OF INVENTION: Recombinant Production of Biologically TILLE OF INVENTION: Active Peptides and Proteins |
| TILLE OF SECURATION: Active Peptides and Proteins |
| TILLE OF SECURATION: Active Peptides and Proteins |
| TILLE OF SECURATION: Active Peptides and Proteins |
| TILLE OF SECURATION: Active Peptides and Proteins |
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| TILLE OF SECURATION: Active Peptides and Proteins |
| TILLE OF SECURATION: Active Peptides and Proteins |
| TILLE OF SECURATION: Active Peptides and Proteins |
| TILLE OF SECURATION: Active Peptides A
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER IN FC compatible
COMPUTER: ABtentin Release #1.0, Version #1.25
SOUTHARE: Patentin Release #1.0, Version #1.25
SOUTHARE: Patentin Release #1.0, Version #1.25
TILNG DATE: 29-401-1994
FLING DATE: 29-401-1994
TILNG DATE: 20-408-400
TELEFRAX: 202-408-400
TELEFRAX: 202-408-4400
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett, ADDRESSEE: Unnner
STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 LeuglyGluArgTyrProlleCysCys 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 44:
Pierce, James C.
Anderson, Mark G.
Kari, Prasad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 108 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.00073
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44.83%
41.88%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1300 I St
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-282-030-45
                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
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2 CysHisCysArgValLeuTyrCysIlePheGlyGluHisLeuGlyGlyThrCysPheIle 21
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PCT-US95-10219-43

Sequence 43, Application PC/TUS9510219

GENERAL INFORMATION:

APPLICANT: Williams, Jon I.

APPLICANT: Pierce, James C.

APPLICANT: Anderson, Mark G.

APPLICANT: Arai, Presad

TITLE OF INVENTION: Recombinant Production of Biologically

TITLE OF INVENTION: Active Peptides and Proteins

NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
                                                                                 COLF: 20003-3415

COLF: 20003-3415

MEDIUM TYPE: Floppy disk
COMPUTER: EM PC compatible
COMPUTER: EM PC compatible
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/282,030
FILING DATE: 29-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PCACHS, Jean B.
REFERENCE/DOCKET NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 30587.0001-00000
TELEPHONE: 202-408-400
TELEPHONE: 202-408-400
TELEFAX: 202-408-4400
TELEFAX: 202-408-400
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-045-180A-6 (1-31) x US-08-282-030-45 (1-108)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1300 I Street, N.W. CITY: Washington
1: D.C.
FRY: USA
20005-3315
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: D.C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
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PCT-US95-10219-44/C

Sequence 44, Application PC/TUS9510219

GENERAL INFORMATION:

APPLICANT: Pierce, James C.

APPLICANT: Arit, Prasad

TITLE OF INVENTION: Recombinant Production of Biologically
TITLE OF INVENTION: Active Peptides and Proteins
NUMBER OF SEQUENCES:

ADDRESSER: Finnegan, Henderson, Farabow, Garrett & ADDRESSER: Dunner

STRERT: 1300 I Street, N.W.

CITY: Washington

CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108
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COUNTRY: U.S.
COUNTRY: U.S.
ZIP: 20005-3315
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: FCT/US95/10219
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                   NAME: Fordis, Jean B.

REGISTRATION NUMBER: 32,984

REGISTRATION NUMBER: 05387.0001-00000

TELECOMMUNICATION INFORMATION:
TELERCOMMUNICATION INFORMATION:
TELERCOMMUNICATION INFORMATION:
TELERCOMMUNICATION INFORMATION:
TELERCOMMUNICATION INFORMATION:
TELERCOMMUNICATION INFORMATION:
TELERCOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 base pairs
TYPE: nucleic acid
STAMDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-045-180A-6 (1-31) x PCT-US95-10219-43 (1-108)
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REGISTRATION NUMBER: 32,984
REFERENCE, DOCKET NUMBER: 05387.0001-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 LeuGlyGluArgTyrProlleCysCys 30
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,030
FILING DATE: 29-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fordis, Jean B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,030
FILING DATE: 29-ULL-1994
ATTORNEY/AGENT INFORMATION:
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80.00
55.17$
44.83$
41.88$
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DB:
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2 CysHisCysArgValLeuTyrCysIlePheGlyGluHisLeuGlyGlyThrCysPheIle 21
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US-08-282-030-61
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Alignment Scores:
Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                Sequence Application PC/TUS9510219

Sequence Application PC/TUS9510219

Sequence Application: Jon I.

APPLICANT: Williams, Jon I.

APPLICANT: Perce, James C.

APPLICANT: Anderson, Mark G.

APPLICANT: Arai, Prasad

TITLE OF INVENTION: Recombinant Production of Biologically TITLE OF INVENTION: Active Peptides and Proteins

NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner

STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: PCT/US95/10219
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                         108
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Mismatches:
Indels:
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                                                                                                                                                                                             Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                        22 LeuglyGluArgTyrProlleCysCys 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 CAGGGTCGTCTGTGGCCATTCTGTTGC 15
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APPLICATION NUMBER: US 08/282,030
FILING DATE: 29-ULI-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Fordis, Jean B.
REGISTRATION NUMBER: 32,984
REPERENCE/DOCKET NUMBER: 05:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 4*
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US95-10219-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 108 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                             0.00073
                                                                                                                                                                                                              80.00
55.17%
44.83%
41.88%
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PCT-US95-10219-45
                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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PCT-US95-10219-45
                                                                                                                                                                           Alignment Scores:
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2 CysHisCysArgValLeuTyrCysIlePheGlyGluHisLeuGlyGlyThrCysPheIle 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Williams, Jon I.
APPLICANT: Williams, Jon I.
APPLICANT: Milliams, Jon I.
APPLICANT: Anderson, Mark G.
APPLICANT: Racce, James C.
APPLICANT: Racce, Mark G.
APPLICANT: Racce, Mark G.
APPLICANT: Racce, Mark G.
TITLE OF INVENTION: Recombinant Production of Biologically
TITLE OF INVENTION: Active Peptides and Proteins
NUMBER OF SEQUENCES: G.
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Pinnegan, Henderson, Farabow, Garrett & CORRESSEE: Dunner
STRATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/282,030
FILING DATE: 29-UTL-1994
CLASSIFICATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 05387.0001-00000
TELLEPHONE: 202-408-4400
INFORMATION FOR #400
INFORMATION FOR #400
INFORMATION FOR #400
INFORMATION FOR #800 #100
INFORMATION FOR #400
INFORMATION FOR #400
INFORMATION FOR #100
INFORMATION FOR #201
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Mismatches:
Indels:
   Length:
Matches:
Conservative:
Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 caggárcercreregecarrcrériec 98
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Patent No. 5589364
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80.00
55.17%
44.83%
0.00073
80.00
55.17%
44.83%
41.88%
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                          Percent Similarity:
Best Local Similarity:
Query Match:
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ACESULT 11
PCT-US95-10219-61/C
; Sequence 61, Application PC/TUS9510219
; General Application PC/TUS9510219
; General Application PC/TUS9510219
; GENERAL INFORMATION:
    APPLICANT: Williams, Jon I.
; APPLICANT: Anderson, Mark G.
; APPLICANT: Anderson, Mark G.
; APPLICANT: Rari, Prasad
; TILLE OF INVENTION: Recombinant Production of Biologically
; TILLE OF INVENTION: Active Peptides and Proteins
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
    ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: D.C.
COMPUTER D.C.
ZIP: 20.005-315
ZIP: 20.005-315
COMPUTER READABLE FORM:
MEDIUM TYPE: F1cppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
SURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10219
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
RIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Fordis, Jean B.
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 05387,0001-00000
TELECOMMUNICATION INFORMATION:
TELEPRONE: 202-408-4000
TELEPRONE: 202-408-4400
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
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55.17%
44.83%
41.88%
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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US-08-021-608D-5/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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891 TGCTATTGCAGAATACCAGCGTGCATTGCAGGAGAACGTCGCTATGGAACCTGCATCTAC 832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
                                                         APPLICANT: LEVENS, DAVID L., DUNCAN,
APPLICANT: ROBERT C., AND AVIGAN, MARK I.
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
CORRESPONDENCE: 24
CORRESPONDENCE: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-045-180A-6 (1-31) x US-08-021-608D-5 (1-1097)
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: WORDPERFECT 5.1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/021,608D
FILING DATE: 22-FEB-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
RERENEK POCKET NUMBER: 2026-4063
TELEPHONE: (212) 758-4800
TELEPHONE: (212) 75-6849
INFORMATION FOR SEQ. ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 LeuGlyGluArgTyrProlleCysCys 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-08-726-160-5/c
; Sequence 5, Application US/08726160
; Patent No. 5734016
; GENERAL INFORMATION:
; APPLICANT: LEVENS, DAVID L., DUNCAN,
                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: FLORPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 5, Application US/08021608D Patent No. 5580760 GENERAL INFORMATION:
                                                                                                                                                                                         ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.00
55.17%
44.83%
41.88%
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TYPE: Nucleic acid
STRANDEDNESS: Double
                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: NC
ANTI-SENSE: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                             10154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; CELL LINE:
US-08-021-608D-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM:
                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
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2 CysHisCysArgValLeuTyrCysIlePheGlyGluHisLeuGlyGlyThrCysPheIle 21
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Matches:
Conservative:
Mismatches:
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                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPEY DISK
MEDIUM TYPE: FLOPEY DISK
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01782
FILING DATE: 22-FEB-1994
CLLASSIFICATION NUMBER: U.S. 08/021,608
FILING DATE: 22-FEB-1993
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 20.26-4063PCT
FILING DATE: 22-FEB-1993
ATTORNEY/AGENT INFORMATION:
FELEPHONE: 758-4600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6849
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 5:
SE
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                   ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE CITY: NEW YORK COUNTRY: NEW YORK COUNTRY: USA ZIP: 10154
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IDENTIFICATION METHOD:
  CORRESPONDENCE ADDRESS:
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POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
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PCT-US94-01782-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Human STRAIN:
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Best Local Similarity:
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DB:
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GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES
APPLICANT: AS REPRESENTED BY THE SECRETARY, DEPARTMENT OF
APPLICANT: HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
APPLICANT: ROBERT C., AND AVIGAN, MARK I.
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: NEW YORK
CITY: NEW YORK
                                                                                                                                                                                                                                US-10-045-180A-6 (1-31) x US-08-726-160-5 (1-1097)
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STRANDEDNESS: Double
TOPOLOGY: Unknown
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: NO ANTI-SENSE: YES ORIGINAL SOURCE: ORGANISM: Human
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Query Match:
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Search completed: December 17, 2003, 14:54:03
Job time : 32 secs
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US-08-282-030-50

i Sequence 50, Application US/08282030

i Sequence 50, Application US/08282030

i Patent No. 558364

i GENERAL INPORMATION:

APPLICANT: Williams, Jon I.

APPLICANT: Malerson, Mark G.

APPLICANT: Rail, Presad

TITLE OF INVENTION: Recombinant Production of Biologically

TITLE OF INVENTION: Recombinant Production of Biologically

TITLE OF INVENTION: Active Peptides and Proteins

NUMBER OF SEQUENCES: 62

CORRESPONDER ADDRESS:

ADDRESSEE: Dunner

STREET: 1300 I Street, N.W.

CITY: Washington

STRATE: 10.C.

COMPITER: Tam PC compatible

COMPUTER: Tam PC compatible

COMPUTER: Patentin Release #1.0, Version #1.25

CORPERATION NUMBER: 32,984

CLASSIFICATION: NUMBER: 32,984

CLASSIFICATION INFORMATION:

NAME: PORTIS, John NUMBER: 32,984

TELEPHONE: 202-408-400

TELEPHONE: 202-408-400

TELEPHONE: 202-408-400

TELEPHONE: ASHARCTERISTICS:

LENGTH: 123 base pairs

TYPE: nucleic acid

TYPE: nucleic acid

TYPE: nucleic acid

SEQUENCE CHARACTERISTICS:

LENGTH: 123 base pairs

TOPOLOGY: 1:nes
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US-08-282-030-50
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Best Local Similarity:
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Pred. No.:
RESULT 15
US-08-282-030-50
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                                                                                                          2003, 14:50:14 ; Search time 20.304 Seconds (without alignments) 445.225 Million cell updates/sec
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94
1 MRTLTLLSAFLLVALQAWAE......GEHLGGTCFILGERYPICCY
                   GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                               283308 seqs, 96168682 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
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Gapop 60.0 , Gapext 60.0
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B450499
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D71984
WTREN1
WTREN1
WTREN5
B01396
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seq length: 2000000000
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                                                                              OM protein - protein search,
                                                                                                             December 17,
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2: pir2:*
3: pir3:*
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Maximum DB :
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hypothetical protection of the 
A32164 A87596 A87596 A379901 A39901 A39901 DVHUCF S223756 D052290 A27290 A27290 A27290 A27290 A27290 A27290 A2730 
EE64660 C69466 C694667 F84689 AF0964 AF0904 T403384 H64796 H64796 F82969 F82969 B85904

A65036 A10115 T26829 C88809 C64509 T38961 AG0854 F84581

C83316 AC1896 D49591 S37434

D90908 F85842 E69079 T12078 Length 94;

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A; Contents: annotation; activation by matrilysin (EC 3.4.24.23) (see PIR:KCHUM). C; Comment: The propeptide is cleaved by matrilysin (EC 3.4.24.23)
                                                                                                                                                                                                                                                                                                                                                                                                                                              F)1.19/Domain: signal sequence #status predicted <SIG>F)20-64/Domain: propeptide #status predicted <PRO>F)56-94/Product: defensin HWP-1 #status experimental <MAII>F)66-94/Product: defensin HWP-2 #status experimental <MAII>F)66-94/Product: defensin HWP-2 #status experimental <MAII>F)66-94,68-83,73-93/Disulfide bonds: #status experimental
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100.0%; Pred. No. 0.5
tive 0; Mismatches
                                                                                      C;Genetics:
A;Gene: GDB:DEFA1; DEF1; MRS; HNP-1
A;Cross-references: GDB:120745; OMIM:125220
A;Map position: 8p23-8p22
A;Introns: 59/1
C;Complex: homodimer
C;Superfamily: mammalian defensin
C;Keywords: antibiotic; homodimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 8; Conservative
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A; Residues: 1-94 <WIE>
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RSG1eted, M. E; Havid, S. S.L.; Ganz, T.; Schilling, J.W.; Lehrer, R.I.
J. Clin. Invest. 76, 1436-1439, 1985
A;Trile: Primary structures of three human neutrophil defensins.
A;Rocession: A30658, MUD:86034582; PMID:4056036
A;Rocession: A30658, MUD:86034582; PMID:4056036
A;Rocession: B30688
A;Rocession: A32958; MUD:89139465; PMID:2917986
A;Title: Determination of the disulfide array in the human defensin HNP-2. A covalently
A;Reference number: A32958; MUD:89139465; PMID:2917986
A;Rocession: A32958; MUD:89139465; PMID:2917986
A;Rocession: A32958; MUD:89139465; PMID:2917986
A;Rocession: A32958; MUD:89139465; PMID:89139465; PMID:862089
A;Rocession: A32958; MUD:89139465; PMID:862089
A;Rocession: A36979; MUD:99139465; PMID:862089
A;Rocession: A56444
A;Rocession: A74769; MUD:991744587
A;Rocession: A74769; MUD:991744587
A;Rocession: A74769; MUD:991744929
A;Rocession: A74769; MUD:991744929
A;Rocession: A74769; MUD:991749; PMID:145897
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A;Rocession: A74769; MUD:991749; PMID:147897
A;Rocession: A74769; MUD:991749; PMID:147899
A;Ritle: Regulation of intestinal 
                                                                                                                                                                                           A40499

A40499

A40499

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Mefensin alpha-1 precursor, myeloid-related [validated] - human

MyAlternate names: defensin HP-1; myeloid leukocyte protein mrs; myeloid-related protein

MyContains: defensin HNP-1; defensin HNP-3

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Date: 24-Jan-1992 #sequence_revision 24-Jan-1892 #text_change 08-Dec-2000

C;Accession: 832499; 807161; A40499; A30658; B30658; A32958; 865412; 865414

R;Linzmeier, R.; Michaelson, D.; Liu, L.; Ganz, T.

R;Linzmeier, R.; Michaelson, D.; Liu, L.; Ganz, T.

A;Title: The structure of neutrophil defensin genes.

A;Reference number: 832499; MUID:99238968; PMID:8477861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S32499
A; Molecule type: DNA
A; Residues: 1-94 ~LIN>
A; Residues: 1-94 ~LIN>
A; Cross-references: GB:L12690; NID:g292362; PIDN:AAA36382.1; PID:g292363
A; Cross-references: GB:L12690; NID:g292362; PIDN:AAA36382.1; PID:g292363
B; Max; W.M.; van Tuinen, P.; Drabkin, H.A.; White, J.W.; Saunders, G.F.
Blood 71, 1713-1719, 1988
A; Title: A myeloid-related sequence that localizes to human chromosome 8q21.1-22.
A; Reference number: S07161; MUID:88222410; PMID:3370315
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A; Residues: 1-94 <MAR>
A; Residues: 1-94 <MAR>
A; Cross -- references: GB: MZ6602; NID: g181528; PIDN: AAA52303.1; PID: g181529
R; Daher, K.A.; Lehrer, R.I.; Ganz, T.; Kronenberg, M.
Proc. Natl. Acad. Sci. U.S.A. 85, 7327-7331, 1988
A; Title: Isolation and characterization of human defensin cDNA clones.
A; Reference number: A40499; MUID: 89017191; PMID: 3174637
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A; Residues: 1-94 < DAH>
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A;Molecule type: protein
A;Residues: 65, X', 67, X', 69-72, X', 74-82 <FRO>
B;Selsted, M.E.; Harwig, S.S.L.
J. Biol. Chem. 264, 4003-4007, 1989
A;Title: Determination of the disulfide array in the human defensin HNP-2. A covalently A;Reference number: A32958; MUID:89139465; PMID:2917986
A;Molecule type: protein
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A;Title: Blochemical and antibacterial analysis of human wound and blister fluid.
A;Reference number: $65409; MUID:96203912; PMID:8620898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-34 cLINA
A;Cross-references: 1-34 cLINA
A;Cross-references: GB:LL12691; NID:9292364; PIDN:AABS7722.1; PID:9292365
R;Wiedemann, L.M.; Francis, G.E.; Lamb, R.F.; Burns, J.H.; Winnie, J.N.; MacKenzie, E.D
Submitted to the EMBL Data Library, November 1988
A;Reference number: $08005
A;Accession: $08005
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A; Residues: 30-94 cDAH-
A; Cross-references: GB: M21131; NID: 9181530; GB: M23281; NID: 9181534; PIDN: AAA52304.1; PI
A; Experimental source: clone HNP-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                defensin alpha-3 precursor, neutrophil-specific [validated] - human N;Alternate names: defensin HNP-3; neutrophil peptide 3 (HNP-3) N;Contains: defensin HNP-2; defensin HNP-3; c;Species: Howo sapiens (man) C;Species: Howo sapiens (man) C;Species: Howo sapiens (man) C;Species: A-Jan-1992 #sequence revision 03-Nov-1995 #text_change 15-Sep-2000 C;Accession: S32500; S08005; E40499; S65413; A32958; C30658 R;Linameier, R.; Michaelson, D.; Liu, L.; Ganz, T. FEBS Lett. 321, 267-273, 1993 A;Fille: The structure of neutrophil defensin genes. A;Fille: The structure of neutrophil defensin genes.
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Bateman A., Singh A., Shustik C., Mars W.M., Solomon S.;
"The isolatrion and identification of multiple forms of the neutrophil granule peptides from human leukemic cells.";
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                    P59665; P1479; Q14125; Created)
01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Neutrophil defensin 1 precursor (HMP-1) (HP-1) (HP1) (Defensin, alpha
1) [Contains: HP 1-56; Neutrophil defensin 2 (HNP-2) (HP2)].
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Selsted M.E., Harwig S.S.L., Ganz T., Schilling J.W., Lehrer R.I.;
"Primary structures of three human neutrophil defensins.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=89139465; PubMed=2917986; Selsted M.E., Harwig S.S.L.; "Determination of the disulfide array in the human defensin HNP-2.
                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=89017191; Pubmed=3174637;
Daher K.A., Lehrer R.I., Ganz T., Kronenber M.;
"Isolation and characterization of human defensin cDNA clones.";
Proc. Natl. Acad. Sci. U.S.A. 85:7327-7331(1988).
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Mars W.M., Vantuinen P., Drabkin H.A., White J.W., Saunders G.E.
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                                                                                                                                                                                                                                                                                                                                 MEDLINE-89142618; PubMed=2918759; Wiedemann L.M., Francis G.B., Lamb R.F., Burns J.H., Winnie McKenzie B.D., Birnie G.D., "Differentiation stage-specific expression of a gene during "Differentiation stage-specific appre
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=96107186; PubMed=8530462; Mars W.M., Patmasiriwat P., Maity T., Huff V., Weil M.M., Saunders G.F.;
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Linzmeier R., Michaelson D., Liu L., Ganz T.;
FEBS Lett. 326:299-300(1993).
             94 AA
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J. Biol. Chem. 264:4003-4007(1989)
                                                                                                                                                                                                                                                                                                Blood 71:1713-1719(1988).
                                                                                                                                                                                                                                                                                                                                                                                    granulopoiesis.";
Leukemia 3:227-234(1989).
                                                                                                         Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-93075734; PubMed-1445873;
Pardi A., Zhang X.-L., Selsted M.E., Skalicky J.J., Yip P.F.;
"NMR studies of defensin antimicrobial peptides. 2. Three-dimensional
structures of rabbit N-2 and human HNP-1.";
Blochemistry 31:11357-11364(1992).
-!- FUNCTION: Defensins 1/2 have antiblotic, fungicide and antiviral
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                  Valore B.V., Ganz T.; "Posttranslational processing of defensins in immature human myeloid
                                                                                                                                             STRUCTURE BY NWR OF DEFENSIN 1.
MEDLINE=33075733; PubMed=1445872;
Zhang X.-L., Selsted M.E., Pardi A.;
"NWR studies of defensin antimicrobial peptides. 1. Resonance
assignment and secondary structure determination of rabbit NP-2 and
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-1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: BELONGS TO THE CORTICOSTATIN/DEFENSIN FAMILY.
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GO; GO:0006935; P:chemotaxis; TAS.
GO; GO:0006955; P:immune response; TAS.
InterPro; IPR006081; Defensin alpha.
InterPro; IPR006080; Defensin_mammal.
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Pfan; PF00879; Defensin_propep; 1.
Pfan; PF00323; defensins; 1.
SMART; SM00048; DEFSN; 1.
                                                                                                                                                                                                                                                                                                     Biochemistry 31:11348-11356(1992).
KEDLINE=92190492; PubMed=1339298;
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Defensin; Antibiotic; Antivira
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EMBL; L12690; AAA36382.1; --
EMBL; X52053; CAA36280.1; --
Genew; HGNC:2761; DEFAI.
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		Description	Q19064 caenorhabdi	Q9ff99 arabidopsis	Q96pl7 homo sapien	O24861 helicobacte	Q9zn45 helicobacte	Q9tu00 macaca mula	Q9ttz9 macaca mula	P82318 macaca mula	Q8ejg5 shewanella		Q98mm4 rhizobium l	Q920n0 tamias sibi	Q9kgw7 pseudomonas	Q9qtd0 marek's dis	Q8ru05 oryza sativ	Q92tq1 rhizobium m
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TISSUE=Liver;
Mata J.F., Garcia-Manteiga J.M., Lostao P., Fernandez-Veledo S.,
Larrayoz I.M., Llobersa J., Casado J., Pastor-Anglada M.;
Larrayoz I.M., Llobersa J., Casado J., Pastor-Anglada M.;
"Role of the human concentrative nucleoside transporter (hCNT1) in the cytotoxic action of 5'-deoxy-5-fluorouridine, an active intermediate metabolite of capecitabine, a novel oral fluoropyrimidine used in
                                                                                                                                       STRAIN=Columbia;
MEDLINE=97471969; PubMed=9330910;
Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
Miyajima N., Tabata S.;
Miyajima N., Tabata S.;
"Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
features of the 1.6 Mb regions covered by twenty physically assigned
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-DBC-2001 (TrEMBLrel. 19, Created)
01-DBC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Concentrative nucleoside transporter 1.
Homo sepiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 7.5;
ive 0; Mismatches 0; Indels
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
BMBL; AR309632; AR109447.1;
Interpro; IRR002668; Nucled transpt2.
Pfam; PF01773; Nucleoside_tra2; 1.
ProDom; PD003768; Nucled transpt2; 1.
                                                                                                                                                                                                                                                                                                         PI CLORGE.";
DNA RES. 4:215-230(1997),
EMBL; AB005244; BAB10054-1; -
InterPro; IPR002422; AA/rel permease2.
InterPro; IPR004242; AA/rel permease2.
Ffam; PP01499; Aa_trans; 1.
PROSITE; PR00309; RNA_RNE 1: 1.
SEQUENCE 467 AA; 51722 MM; 1BB41C85CE364406 CRC64;
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SEQUENCE 649 AA; 71598 MW; DCD4EA8F585A00CD CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
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                       eurosids II; Bra.
NCBL TaxID=3702;
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Q9wzk4 thermotoga
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        Q47664 escherichia
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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Waterston R.;
"Direct Submission.";
Submitted (UN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; US943; AAA68364.1; -.
WormPep; E0466.9; CE01221.
Hypothetical protein.
SEOUENCE 128 AA; 13694 MW; 7BBAF31DB567ACEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pauley A.;
"The sequence of C. elegans cosmid E04F6.";
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
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STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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ABU04826 ABU04831 ABU04803 ABU04805 ABU04806 ABU04808 ABU04835 ABU04838 AAR22318 AAR22318 AAR22318 AAR22318 AAR2244 AAR34959 AAR34959 AAR34959 AAR34959 AAR34959 AAR34959	ALIGNMENTS	94 AA.			the human defensin (Def-X)	Human defensin, Def-X, antimicrobial, ar cytostatic, anticancer, inflammation, trendocrine regulation, corticostatic regAIDS; immune deficiency; psoriasis.									Def-X - useful		represents human de led as an antimicrol X polypeptide can land and and as an		2 2 4	or spirochaete infeted with enveloped	
2444444444 44444444				<u>S</u> .	he h	ntim infl rtic pso				823.	823.		'n		de D ide,	French	rese as a olyp agen	ide in a	used , es tive	Spi d wi d fo	
W R W W W W W W W W W W W W W W W W W W		standard; protein;		st entry)	ce of t	ef-X; a ancer; ion; co ciency;				97FR-0010823	97FR-0010823		Chumakov	16.	polypeptide D t, pesticide,	56pp; Fr	nce rep e used Def-X p ancer)	olypept cially	can be ections am-posi	fungal or associated is can used	melanomas, or
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~		lard		(first	sequence	n, D ntic ulat defi				97	97	T SA		266/1		1; 5	sequence can be u The Def anticanc	he pespe	r. ging	, fu e as ons	Tanc
			3;	-1999	acid se	lefensi ttic; a: ne regi	sapiens.	32-A1.	1999.	1997;	1997;	GENSET	eret L	999-183	F .	1; Fig	present so peptide ca sticide. '	ion. T	ning De casitic lons ar	mycobacterial, fur infections are ass The compositions	алу ше
88888888888888888888888888888888888888		RESULT 1 AAY01603 ID AAY01603	AC AAY01603	18-JUN				AA PN FR2767832 XX	PD 05-MAR-	PF 29-AUG-	PR 29-AUG-	PA (GEST )	PI Bouguel	WPI; 1	Human antica	Claim	C. The present sequence represents human CC polypeptide can be used as an antimit CC a pesticide. The Def-X polypeptide can (especially anticancer) agent, and an consist of inflammation tions.				d a a

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polypeptide can be used as an antimicrobial, antiparasitic agent or a pesticide. The Def-X polypeptide can be used as a cytostatic agent or cespecially anticancer) agent, and as an agent for modulating processes of inflammation, tissue repair and endocrine (especially corticostatic) regulation. The polypeptide can be used in a composition for external topical use, especially in a cosmetic composition. Compositions containing Def-X can be used for prevention and treatment of microbial and parasitic infections, especially where the microbial or parasitic infections are Gram-positive or -negative bacterial infections or mycobacterial, fungal or spirochaete infections, or where the viral infections are associated with enveloped viruses, especially HSV and HIV. The compositions can used for prevention and/or treatment of cancers, especially melanomas, or liver cancer, prostate cancer, non-small-cell lung cancer or colorectal carcinoma, and for enhancing immunity,
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lung cancer or colorectal carcinoma, and for enhancing immunity, especially in the case of AlDS, or preventing immune deficiency, especially in the treatment of psoriasis, as well as for modulating inflammatory processes, especially in the case of chronic inflammatory
                                                                                                                                                                                                          1 MRTLTLLSAFLLVALQAWAEPLQARAHEMPAQKQPPADDQDVVIYFSGDDSCSLQVPGST
                                                                                                                                                                                                                              1 MRTITILSAFILVALQAWAEPLQARAHEMPAQKQPPADDQDVVIYFSGDDSCSLQVPGST
                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human defensin; Def-X; antimicrobial; antiparasitic; pesticide; cytostatic; anticancer; inflammation; tissue repair; endocrine regulation; corticostatic regulation; cancer; melanoma; AIDS; immune deficiency; psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents human defensin (Def-X). The Def-X

    useful as antimicrobial agent,

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                                                                                                                                        Length 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of the human defensin (Def-X) protein.
                                                                                                                                                                        Indels
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                                                                                                                                      100.0%; Score 94; DB 20;
100.0%; Pred. No. 2.5e-91;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                             94
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                                                                                                                                                                                                                                                                                                  KGLICHCRVLYCIFGEHLGGTCFILGERYPICCY
                                                                                                                                                                                                                                                                               KGLICHCRVLYCIFGEHLGGTCFILGERYPICCY
                                                                                                                                                                                                                                                                                                                                                                                                   AAY01604 standard; protein; 94 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human defensin polypeptide Def-X anticancer agent, pesticide, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Fig 3; 56pp; French
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                        94; Conservative
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                                                                                                                                                        Similarity
                                                                                                      94 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAX26697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bougueleret L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo gapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FR2767832-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JUN-1999
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                                                                    disorders.
                                                                                                                                                                                                                                                                               61
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                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY01604;
                                                                                                        Sequence
                                                                                                                                      Query Match
Best Local
                                                                                                                                                          Best Loca
Matches
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Length 31;

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inflammatory processes, especially in the case of chronic inflammatory
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                                      31 AA;
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                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-2001.
                                                                                        31;
             disorders.
                                      Sequence
                                                                                                                                                                                                                                   ABB44491;
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                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents human defensin (Def-X) fragment. The Def-X polypeptide can be used as an antimicrobial, antiparametric agent or a pesticide. The Def-X polypeptide can be used as a cytostatic agent (especially anticancer) agent, and as an agent for modulating processes of inflammation, tissue repair and endocrine (especially corticostatic) regulation. The polypeptide can be used in a composition for external contraining Def-X can be used for prevention and treatment of microbial containing Def-X can be used for prevention and treatment of microbial and parametric infections, especially where the microbial or paramitic infections are associated with enveloped viruses, especially HSV and HIV.

The compositions can used for prevention and/or treatment of cancers, compositions or used for prevention and/or treatment of cancers, compositions or used for prevention and/or treatment of cancers, compositions or liver cancer, profette cancer, non-small-cell ung cancer or colorectal carcinoma, and for enhancing immunity, especially in the treatment of psoriamis, as well as for modulating
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especially in the case of AIDS, or preventing immune deficiency, especially in the treatment of psoriasis, as well as for modulating inflammatory processes, especially in the case of chronic inflammatory
                                                                                                                                                           1 MRILILISAFILVALQAWAEPLQARAHEMPAQKQPPADDQDVVIYFSGDDSCSLQVPGST
                                                                                                                                           1 MRTLTLLSAFLLVALQAWAEPLQARAHEMPAQKQPPADDQDVVIYFSGDDSCSLQVPGST
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                        Human defensin, Def-X, antimicrobial, antiparasitic; pesticide, cytostatic; anticancer; inflammation; tissue repair; endocrine regulation, corticostatic regulation; cancer; melanoma; AIDS; immune deficiency; psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human defensin polypeptide Def-X - useful as antimicrobial agent,
                                                                                                                   ö
                                                                                         Length 94;
                                                                                                                  0; Indels
                                                                                       100.0%; Score 94; DB 20;
100.0%; Pred. No. 2.5e-91;
live 0; Mismatches 0;
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                                                                                                                                                                                                             KGLICHCRVLYCIFGEHLGGTCFILGERYPICCY
                                                                                                                                                                                            61 KGLICHCRVLYCIFGEHLGGTCFILGERYPICCY
                                                                                                                                                                                                                                                                                                                                                                  Fragment of human defensin (Def-X) protein.
                                                                                                                                                                                                                                                                                       AAY01606 standard; peptide; 31 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anticancer agent, pesticide, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Page 33; 56pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97FR-0010823.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chumakov I;
                                                                                                                                                                                                                                                                                                                                          18-JUN-1999 (first entry)
                                                                                                                   94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-183266/16.
                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GEST ) GENSET SA.
                                                                   94 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bougueleret L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-MAR-1999
                                         disorders.
                                                                   Sequence
                                                                                                                                                                                                                                                                                                                AAY01606;
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Best Local (
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
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100.0%; Pred. No. 1.2;
                                                                    0; Indels
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                Score 31; DB 20; I Pred. No. 3.2e-25;
33.0%; Sco...
100.0%; Pred. No. 5...
0; Mismatches
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Local Similarity 100.0%; Pred. NO. ...
                                                                                                                                                     1 ICHCRVLYCIFGEHLGGTCFILGERYPICCY 31
                                                                                                                       94
                                                                                                                     64 ICHCRVLYCIFGEHLGGTCFILGERYPICCY
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                                                                                                                                                                                                                                                                                                           ABB44491 standard; Peptide; 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Penn SG, Hanzel DK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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AAU32095;

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probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human peptide encoded by genome-derived single exon probe SEQ ID 36921.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chronic obstructive pulmonary disease; interstitial lung disease, familial idiopathic pulmonary fibrosis; neurofibromatosis; tubercus sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiccytosis; lumphangioleiomyomicosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of single exon nucleic acid
                                                          Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma.
                  Human bone marrow expressed probe encoded protein SEQ ID NO: 38550.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; SEQ ID NO: 38550; 658pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; single exon probe; asthma; lung cancer; COPD; ILD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein encoded by one of the probes of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                          30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
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                                                                                                                                                                                                                                                                                                                                                                                                                                27-SEP-2000; 2000US-0236359
                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-OCT-2000; 2000GB-0024263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 AEPLQARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 AA;
                                                                                                                                                                              WO200157276-A2
                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                       26-MAY-2000;
30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptides weeters comprising the nucleic acids encoding the polypeptides and cells genetically the proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to have a set and in the processing the proteins are useful in genetic vaccination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AANI29310-AAJ33304 represent the amino acid sequences of novel human secreted proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of human polypeptides, useful in genetic
                                                                                                                                                                                                                                             Human, vaccination, gene therapy, nutritional supplement;
stem cell proliferation; haematopoiesis, nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
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Local Similarity 100.0%; Pred. No
les 8; Conservative 0; Mismat
                                                                                                                                                                                                        Novel human secreted protein #2586.
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                                                                 AAU32095 standard; Protein; 58 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drmanac RT;
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26-JAN-2001; 2001US-0770160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-APR-2001; 2001WO-US08656.
                                                                                                                                                           (first entry)
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RESULT 5
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ID AAU32095
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XX BAU32
XX BAU33
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06-NOV-2001

AAM78244;

AAM78244 ID AAM7 XX AC AAM7 XX DT 06-1

RESULT 6

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Sequence

Query Match

Title: Perfect score:

Sequence:

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OM protein

Run on:

Scoring table:

Word size :

Searched:

Minimum DB 8 Maximum DB 8

Database

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Sequence 123, App Sequence 22, Appli Sequence 24, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appl Sequence 10, Appl Sequence 11, Appl Sequence 169, App Sequence 169, App Sequence 169, Appl Sequence 169, Appl Sequence 169, Appl Sequence 11, Appl Sequence 13, Appli Sequence 27, Appli Sequence 130, Appli Sequence 125, Appli Sequence 126, Appli Sequence 127, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 28, Appl Sequence 28, Appl Sequence 1191, Appl Sequence 28, Appl Sequence 28, Appl Sequence 28, Appl Sequence 28, Appl Sequence 1191, Appl Sequence 28, Appl Sequen
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US-10-367-169-2
US-10-118-471-28
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Sequence 5, Appli
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Sequence 65, Appli
                                                                                           ; Search time 37.6 Seconds (without alignments)
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1: /cgn2_6/ptodata/1/pubpaa/PtoTPUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PtoTNEM_PUB.pep:*

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4: /cgn2_6/ptodata/1/pubpaa/USOG_NEW_PUB.pep:*

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                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-045-180A-3

US-10-045-180A-5

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US-10-013-770-4

US-10-045-180A-4

US-10-141-445-12

US-10-141-645-12

US-10-141-645-12

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                                                                                              December 17, 2003, 14:51:01
                                                                      protein search, using sw model
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4444EE11 4444EE10 68888

Score

Result No.

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Sequence 3, Application US/10045180A;

j Sequence 3, Application US/10045180A;

j Sequence 3, Application No. US20020182703A1

j GENERAL INFORMATION:

j APPLICANT: Bouguelerer, Lydie

j APPLICANT: Chumakov, Ilya

j TITLE OF INVENTION: Containing Them and Applications to Diagnosis and to Therapeutic

j TITLE OF INVENTION: Containing Them and Applications to Diagnosis and to Therapeutic

j TITLE OF INVENTION: Containing Them and Applications to Diagnosis and to Therapeutic

j TITLE OF INVENTION: UNMBER: US/10/45,180A

CURRENT FILING DATE: 2000-02-25

PRIOR FILING DATE: 1998-09-28

PRIOR FILING DATE: 1997-08-29

NUMBER OF SEQ ID NOS: 12

SEQ ID NO 3

LENGTH: 94

LENGTH: 94
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                   MRTLTLLSAFLLVALQAWAEPLQARAHEMPAQKQPPADDQDVVIYFSGDDSCSLQVPGST
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC_FEATURE
OCTHER INFORMATION: Def-X preproprotein sequence
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(19)
OTHER INFORMATION: Def-X signal peptide
FRATURE:
NAME/KEY: PROPEP
ICCATION: (20)...(63)
OTHER INFORMATION: Def-X propeptide
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Best Local Similarity 100.0%; Pred. No. 1.8e-88;
Matches 94; Conservative 0; Mismatches 0;
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NAME/KEY: PEPTIDE
LOCATION: (64)..(94)
OTHER INFORMATION: Def-X mature peptide
US-10-045-180A-3
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                                Sequence 7570, Ap
Sequence 351, App
Sequence 4179, Ap
Sequence 6179, Ap
Sequence 163, Appl
Sequence 37898, A
Sequence 1378911
Sequence 133, Appl
Sequence 133, Appl
Sequence 133, Appl
Sequence 4, Appli
                                                                                                                                                                                                                                                                                                     RESULT 1
US-10-013-770-3
US-110-013-770-3
SEQUENCE 3, Application US/10013770
; Publication No. US20020115151A1
; GENERAL INFORMATION:
; APPLICANT: GENSET SA
; TITLE OF INVENTION: HUMAN DEFENSIN DEF-X GENE AND DNAC
; TITLE OF INVENTION: HUMAN DEFENSIN DEF-X GENE AND DNAC
; TITLE OF INVENTION: HUMAN DEFENSIN DEF-X GENE AND DIAGNOSTIC AND
; THERAPEUTIC APPLICATIONS
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION DATA:
PFLING DATE: 10-Dec-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 94; DB 14; Length 94; 100.0%; Pred. No. 1.8e-88;
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ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 550 West C Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
2 US-10-262-439-81

5 US-10-218-654-81

5 US-10-10-67-17-570

6 US-10-080-170-351

0 US-09-895-298-62

1 US-09-895-298-62

1 US-09-864-761-37898

US-10-080-113-2

US-09-864-133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Hart, Daniel
REGISTRATION NUMBER: 40,637
REFERENCE/DOCKET NUMBER: GENSET.064C1
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 94 AMINO ACIDS
                                                                                                                                                                                              US-09-798-029-4
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FILING DATE: <Unknown>
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SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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20..63
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STATE: California
COUNTRY: USA
ZIP: 92101
COMPUTER READABLE FORM:
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Best Local Similarity
Matches 94; Conserv
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S-09-198-452A-377
S-08-602-725-32
S-08-217-299-1
S-08-602-725-36
5169835-17
US-09-252-91A-30414
US-09-252-91A-30414
US-09-1918-452A-377
US-08-612-725-36
US-08-62-725-36
US-08-62-725-36
US-08-6389-452A-17
US-08-931-912-4
US-09-911-912-4
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US-09-426-42-42
US-09-426-42-42
US-09-426-42-40-81
US-09-426-42-40-81
US-09-426-542-19
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Sequence 5,
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/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-158-189-12
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US-08-158-189-1
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                                                                                                                                                                                                Sequence 3, Application US/09486580A
| Patent No. 6329340
| GENERAL INFORMATION:
| TITLE OF INVENTION: HUMAN DEFENSIN DEP-X GENE AND DNAC
| TITLE OF INVENTION: THERAPEUTIC APPLICATIONS
| TITLE OF INVENTION: THERAPEUTIC APPLICATIONS
| WIMBER OF SEQUENCES: 6 CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Knobbe, Martens, Olson & Bear STREET: 550 West C Street
| CITY: San Diego.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDITAL TYPE: Ploppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: DEACHLINE PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/486,580A

FILING DATE: PEBRINZY 25, 2000

ATTORNEY/AGENT INPORMATION:

NAME: Hart, Daniel

REFERENCE/DOCKET UNDBER: GENSET.064C1

INPORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 94 AMINO ACIDS

TYPE: MINO ACIDS

TYPE: MINO ACIDS

TYPE: AMINO ACIDS

TYPE: MINO ACIDS

TYPE: MINO ACIDS

TYPE: MINO ACIDS

TYPE: AMINO ACID
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MOLECULE TYPE: PROTEIN
ORIGINAL SOURCE:
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MEDIUM TYPE: Floppy
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RESULT 2
US-09-486-580A-5
US-09-486-580A-5
; Sequence 5, Application US/09486580A
; Patent No. 6329340
; GENERAL INFORMATION:
; APPLICANT: GENSET SA

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Gaps
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GENERAL INDORMATION:
APPLICANT: GENES SA
APPLICANT: GENES SA
TITLE OF INVENTION: HUMAN DEFENSIN DEF-X GENE AND DNAC
TITLE OF INVENTION: COMPOSITION CONTAINING SAME AND DIAGNOSTIC AND
TITLE OF INVENTION: THERAPEUTIC APPLICATIONS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
  HUMAN DEFENSIN DEF-X GENE AND DNAC COMPOSITION CONTAINING SAME AND DIAGNOSTIC AND THERAPEUTIC APPLICATIONS
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/486,580A
FILING DATE: FEBRURY 25, 2000
ATTORNEY/AGENT INFORMATION:
NAME: Hart, Daniel
REGISTRATION NUMBER: 40,637
REFERENCE/DOCKET NUMBER: GENSET.064C1
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB 4; Le
Pred. No. 1.9e-39;
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TITLE OF INVENTION: HUMAN DEFENSIN DEF-X GENE TITLE OF INVENTION: COMPOSITION CONTAINING SALTILE OF INVENTION: THERAPEUTIC APPLICATIONS NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS: ADDRESSEE: Knobbe, Martens, Olson & Bear STRET: 550 West C Street
CITY: San Diego STATE: California
COUNTRY: USA
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100.0%; Pred. No. 1...
0; Mismatches
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Best Local Similarity
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30 31 32 33 34 34 35 36 36	tes/sec ,	4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	ance to have a established, being printed, 65 cibution.  Description
re version 5.1.6 93 - 2003 Compugen Ltd.  sw model 14:50:14 ; Search time 6.696 Sec (without alignments)	445.225 TCFILGERYPICCY 60.0	chosen parame	results predicted by charto the total score distinct the total score di
GenCo Copyright (c) 19 OM protein - protein search, using Run on: December 17, 2003,	Title: Perfect score: 31 Sequence: Scoring table: OLIGO Gapop 60.0 , Gapext Searched: 283308 segs, 961686	ord size:  otal number of hits satisfying inimum DB seq length: 0 aximum DB seq length: 200000000 ost-processing: Listing first latabase:  1: pir:* 2: pir:* 3: pir:* 4: pir:*	Result Query analysis and is derived by analysis of 19.4 [15.1]  Score Match Length DB [19.4 [13.1]  Score Match Length DB [19.4 [13.1]  Score Match Length DB [19.4 [13.1]  Score [19.4

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R;Sawada, K.; Agata, K.; Eguchi, G.
Exp. Eye Res. 55, 879-887, 1992
A;Title: Crystallin gene expression in the process of lentoidogenesis in cultures of ch
A;Reference number: A49181; MUID:93137981; PMID:1283129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-137 <COL>
A;Cross-references: GB:Z80775; GB:AL123456; NID:G3250715; PIDN:CAB02528.1; PID:G1568588
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A;Authors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                         ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A,Recerence number: AB2577; MUID:21608550; PMID:11743193
A,Accession: AG3198
A,Status: preliminary
                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE008687; PIDN:AAL46005.1; PID:g17743760; GSPDB:GN00188
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Myčobacterium tubercúlosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
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C;Species: Gallus gallus (chicken)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
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A,Moleoule type: nucleic acid
A,Residues: 1-174 <SAN>
A,Cross-references: GB:S53164; NID:g263999; PIDN:AAB25041.1; PID:g264000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein Rv0049 - Mycobacterium tuberculosis (strain H37RV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: Rv0049
C;Superfamily: Mycobacterium tuberculosis hypothetical protein Rv0049
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100.0%; Pred. No. 20;
tive 0; Mismatches
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19.4%; Score 6; DB 2.
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                      A; Molecule type: DNA A; Residues: 1-131 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: Atu5317
A;Genome: plasmid
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A,Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                               hypothetical protein MJ0039 - Methanococcus jannaschii
c;Species: Methanococcus jannaschii
C;Accession: G64304
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R; Rixhness, B.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Freich, C.J.; Overbeek, R.; Kirkness, B.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, CA; Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A;Reference number: A64300; MUD:96337999; PMID:8688087
A;Accession: G64304
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-115 < BULD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross.references: GB:U67462; GB:L77117; NID:g1590835; PIDN:AAB98020.1; PID:g1590840;
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:ive 0; Mismatches
                  ALIGNMENTS
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A;Start codon: TTG
C;Superfamily: RNA polymerase, subunit F
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PRO1 MALDO
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(c) 1993 - 2003 Compugen Ltd.
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CRAB_CHICK
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EFFGZ_SCHPO
LRPZ_HUMAN
PHYB_ASPPI
CRAB_TRASC
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Match Length
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                                                                                                                                                        NECULINE 97271643; PubMed=9126559;
MEDLINE=97271643; PubMed=9126559;
Casppers G.J., Ult de Weerd D., Wattel J., de Jong W.W.;
"Alpha-crystallin sequences support a galliform/anseriform clade.";
Mol. Phylogenet. Evol. 7:185-188 (1997).
-i. FUNCTION: MAY CONTRIBUTE TO THE TRANSPARENCY AND REFRACTIVE INDEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                         SUBUNIT: AGGREGATES WITH HOMOLOGOUS PROTEINS, INCLUDING ALPHA-A-CXYSTALLIN AND THE SMALL HEAT SHOCK PROTEIN HSP28, TO FORM LARGE HETEROMERIC COMPLEXES.
SIMILARITY: BELONGS TO THE SMALL HEAT SHOCK PROTEIN (HSP20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIINE=97271643; PubMed=9126559;
Caspers G.J., Uit de Weerd D., Wattel J., de Jong W.W.;
"Alpha-crystallin sequences support a galliform/anseriform clade.";
Mol. Phylogenet. Evol. 7:185-188 (1997).
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                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Ayes; Neognathae; Columbiformes; Columbidae; Columba
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15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alpha crystallin B chain (Alpha(B)-crystallin) (Fragment).
                                   15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Alpha crystallin B chain (Alpha(B)-crystallin) (Fragment)
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100.0%; Pred. No. 5.7;
tive 0; Mismatches
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              52 AA.
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ProDom; PD001193; crystallin N; 1.
PROSITE; PS01031; HSP20; PARTIAL.
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InterPro, IPR003090; Crystallin_N.
InterPro, IPR002068; Hsp20.
                PRT;
                                                                                                Columba livia (Domestic pigeon)
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                STANDARD;
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les 6; Conserv
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52 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eye lens protein.
                                                                                                                                    NCBI_TaxID=8932;
                                                                                                                                                                                                                                 OF THE LENS
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012995;
                                                                                                                                                                                                                                                                                           FAMILY.
                 COLLI
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SEQUENCE
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Matches
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    CRAB COLLI
                 CRAB
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAINEJAL-1 / DSW 2661 / ATCC 43067;
STRAINEJAL-1 / DSW 2661 / ATCC 43067;
MIDDLINE=96337999; PubMed=868087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlawage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kalley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
FUNCTION: MAY CONTRIBUTE TO THE TRANSPARENCY AND REFRACTIVE INDEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                       SUBUNIT: AGGREGATES WITH HOMOLOGOUS PROTEINS, INCLUDING ALPHA-A-CRYSTALLIN AND THE SMALL HEAT SHOCK PROTEIN HSP28, TO FORM LARGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                              HETEROMERIC COMPLEXES.
SIMILARITY: BELONGS TO THE SMALL HEAT SHOCK PROTEIN (HSP20)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 AA; 6143 MW; 82271ECE2619EF6F CRC64;
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.4%; Score 6; DB 1;
100.0%; Pred. No. 5.7;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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InterPro; IPR002068; HSp20.
Bfam; PF00525; crystallin; 1.
ProDom; PD001193; Crystallin N; 1.
PROSITE; PS01031; HSP20; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Last an
Hypothetical protein MJ0039.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X96595; CAA65413.1; -
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hes 6; Conservative
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NON_TER 1
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SRQUENCE 52 AA;
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                                         THE LENS
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Y039 METJA
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Matches
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Run

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Quecijs mycobacceri
QBEGGS mycobacceri
QBENIUD bathyerque
QBKIU2 terreptomyce
QBKIU2 terreptomyce
QBKIU2 thryonomys
QBKIU2 thryonomys
QBKIU2 thryonomys
QBKIU2 thryonomys
QBKIU3 caenorhabdi
O01412 onchocerca
QBGSB rhizobium 1
QBIBS caenorhabdi
O01412 onchocerca
QBBCSB rhizobium 1
QBIBS caenorhabdi
QBISS caenorhabacte
O32041 bacillus su
QBEQB rhizobacteri
QBISS carnebacte
O32041 bacillus su
QBEQB araja eglant
QBISS carnebacte
O31142 onchocerca
QBEQBS carnebacte
O31142 chizobacteri
QBEQBS carnebacte
QBEQBS carnebacte
QBISSI xenopus lae
QBISSI xenopus a
QBISSI actococcus
QBICSI mas musculu
QBDAS lactococcus
QBCCI mas musculu
QBOSTI homo sapien
QBCCI mas musculu
QBOSTI trizobium m
QBCCI harbidopsis
QBCSTI sulfolobus
QBCSTI sulfolobus
QBCSTI sulfolobus
QBCSTI sulfolobus
QBCSTI sulfolobus
QBCSTI aulfolobus
                                                                               Q8Ewc8 methanopyru
Q98iz0 rhizobium 1
Q9as6 caulobacter
Q2Fju4 streptomyce
Q989g1 rhizobium 1
Q9z7w8 chlamydia p
Q9x2d1 chlamydia p
Q9x2d1 chlamydia p
Q8xq4 mycobacteri
Q0S898 mycobacteri
Q0S898 mycobacteri
Q0S898 mycobacteri
Q8wrt0 megaderma 1
Q9b8w5 taenia cras
Qm6k9 taenia soli
Q9b8y4 fasciola he
Q34521 fasciola he
Q92aw6 listeria in
Q8y6j0 listeria mo
Q8vgp0 mus musculu
O59869 orpinomyces
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Q93519 salmonella
Q05625 staphylococ
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O57699
P89500
Q96V76
Q8FE45
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Q40942
P88955
Q38295
Q9QTZ3
Q8F683
Q8GYC8
Q92WF2
         Q8M6K9
Q9B8Y4
Q34521
Q92AW6
Q8Y6J0
Q8VGP0
                                                                                                                         Q989G1
Q927W8
Q9E7W8
Q8EQ89
Q8ERQ4
O05898
Q8EMTO
Q8ESQ6
Q8CJT2
Q8CJT2
Q8CJT2
Q8CJT2
Q8CJT2
Q8CJT2
Q8CJT2
Q8CJT2
Q8CJT2
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Q25631
Q25631
Q9EUL7
Q9BL89
Q911D6
Q9UF94
Q911D6
Q9UF94
Q9UF94
Q9UF94
Q9UF94
Q9UF94
Q9UF94
Q9UF97
Q8F71
Q8F71
Q8F71
Q8F52
Q9DEF0
Q6BES2
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Q935L9
Q05625
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Q981Z0
Q9AA86
Q9RJU4
                                                                       059869
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Q8j31 ficedula hy
Q8yg5s vibrio chol
Q8uk07 agrobacteri
O69489 mycobacteri
Q8xed5 taenia soli
Q8xed3 salmonella
Q8xq5 drosphales g
Q90277 brachydanio
Q97453 drosophila
Q97629 clostridium
Q99815 staphylococ
Q46029 citrobacter
Q95813 hymenolepis
Q8m675 paragonimus
Q8m675 paragonimus
                                                                        ; Search time 14.632 Seconds (without alignments) 546.722 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                              830525
             GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                               US-10-045-180A-6
31
1 ICHCRVLYCIFGEHLGGTCFILGERYPICCY :
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                                                                        2003, 14:50:14
                                                     sw model
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Q8JJJJ
Q8KQ95
Q8UKO7
Q8JB9
Q8KBB3
Q8KBB3
Q8KBB3
Q9VA75
Q9VB37
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sp_human:*
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_bacteriap:*
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                                                      using
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                                                     - protein search,
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                        Copyright
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Match
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Gaps

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MEDLINE=20406833; PubMed=10952301; MEDLINE=20406833; PubMed=10952301; MEDLINE=20406833; PubMed=10952301; Melson W.C., Clayton R.A., Gwinn M.L., Dodson R.J., Hafeky E.K., Peterson J.D., Umayam L.A., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D., Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P., McDonald L., Utterback T., Pleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Praser C.M.;
"Single-nucleotide polymorphism characterization in species with limited available sequence information; high nucleotide diversity revealed in the avian genome."; Mol. Ecol. 11:603-612(2002).

EMBL; AF454242; AAM22921.1; -.

EMBL; AF454242; AAM22921.1; -.

Prepom; PF00525; crystallin, 1.

Probom; PF001193; Crystallin, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.";
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Vibrionaceae; Vibrio.
NCBL_TaxID=666;
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TIGR; VC2105; -.
Hypothetical protein; Complete proteome.
SEQUENCE 124 AA; 14590 MW; 6E68B678976CBBF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATUS317.
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Plasmid AT.
                                                                                                                                          39 AA; 4442 MW; 24034FE4C5BD1E55 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein Atu5317.
                                                                                                                                                                                                                                                                                                                                                 01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical protein VC2105.
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                                                                                                                                                                                                                                                                                                                            PRT;
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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NON TER
SEQUENCE
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Q9KQ95;
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Matches
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                                                                                                  Q94uz4 gracula rel
Q8ske8 gracula rel
Q8zi77 yersinia pe
Q8x1m0 calonectria
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0
                              Q93vwl oryza sativ
O43207 homo sapien
Q8h9y3 pseudomonas
                                                                        Q98955 mesembryant
Q9dhu7 yaba-like d
     Q8x1m4 calonectria
Q8x1m2 calonectria
                                                                                                                                                                                                                                                                                                                                                    Ficedula albicollis.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ficedula hypoleuca.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primmer C.R., Borge T., Lindell J., Saetre G.-P.;
"Single-nucleotide polymorphism characterization in species with
"Single-nucleotide polymorphism characterization in species with
"Imited available sequence information: high nucleotide diversity
revealed in the avian genome.";
Mol. Ecol. 11:603-612(2002).
EMBL; AF454243; AAM22922.1;
Interpro; IPR00309; Crystallin N.
Probom; PP001193; Crystallin, 1.
Probom; PD001193; Crystallin N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 AA; 4442 MW; 24034FE4C5BD1E55 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                   QBJJ30;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Spl;
MEDLINE=21918460; PubMed=11918793;
Primmer C.R., Borge T., Lindell J., Saetre G.-P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
19.4%; Score 6; DB 13
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 AA
                                                                                                                                                                                     ALIGNMENTS
                                                                      Q9S955
Q9DHU7
Q94UZ4
                               Q93VW1
Q43207
Q8H9Y3
                                                                                                                              082177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21918460; PubMed=11918793;
                                                                                                                 Q8SKE8
                                                                                                                                           Q8X1M0
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                                                                                                                                                                                                                                                                                                                       Alpha-B-crystallin (Fragment)
ABC.
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110
112
16
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                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 iFGEHL 17
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                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=59894;
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     NON_TER
NON_TER
SEQUENCE
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Q8JJ31
ID Q8JJ31
DT Q1-Q
DT 01-O
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DT 01-O
DE ABC
OC APC
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Proceeding services with the services of 5.1.6   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0   1.0	Human liver peptid Peptide #4710 enco Peptide #4813 enco Protein #4599 enco Human brain expres Human bone marrow Peptide #4710 enco Peptide #4802 enco Peptide #4570 enco	Human ceptide enco Functothenate kinas Drosophila melanog Novel human diagno Haemophilus influe Listeria monocytog Chlamydia pneumoni Lettuce big-vein v Mycobacterium tube Haemophilus influe Haemophilus influe Haemophilus influe Rovel human diagno Novel human diagno Pseudomonas aerugi Drosophila melanog Human grotein phos Fseudomonas aerugi Human calcium sensi	Human placental ca Human placental ca Human nalcium sens Human placental ca Human placental ca Human placental ca Human parathyroid Human parathyroid Human marathyroid Human marathyroid Human Berzeted pro Insulin/insulin-li Secreted protein e Human secreted pro Insulin/insulin-li Secreted protein Human S' EST secre LDHC_XENIA position Human pancreatic c Ddcdc2 positions p Human musculoskele Human musculoskele Human ORF3091 prot Human ORF218 protein Human ORF218 protein	Propionibacterium Novel human diagno Peptide #5542 enco Human brain expres Human bone marrow Peptide #5490 enco Human peptide enco Human immune/haema Human nrostate spe Human prostate spe Human prostate spe Human prostate spe Human prostate spe Human ovarian anti Human immune/haema Drosophila melanog Propionibacterium Human immune/haema Drosophila melanog Propionibacterium Human immune/haema
Copyright (c) 1933 - 2000 Compagen Ltd.  Locamber 17, 2003, 14:50:14; Search time 18:352 Seconds  20:10-045-180A-6  11 CICHCWINCYPERILOROFFILGERVFICCY 31  LOCAMON AND AND AND AND AND AND AND AND AND AN	19.4 179 22 19.4 179 22 19.4 179 22 19.4 179 22 19.4 179 22 19.4 179 22 19.4 179 22 19.4 179 22 19.4 179 22	199.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.	199.4 199.4 199.4 199.4 199.4 199.4 199.4 199.4 199.4 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 199.5 19	16.1 16.1 16.1 16.1 16.1 16.1 16.1 16.1
GenCore versi  Copyright (c) 1993 - 200  Lein search, using sw mode  December 17, 2003, 14:50:1  US-10-045-180A-6  31 ICHCRVLYCIFGEHLGGTCFILGE  OLIGO  Gapop 60.0, Gapext 60.0  1107863 seqs, 158726573 re  0  hits satisfying chosen par  ength: 0  Eisting first 100 summari  A Geneseq 19Jun03:*  B Geneseq 19Jun03:*  A Geneseq 19Jun03:*  B Geneseq	2 Seconds	updates/sec	*****	chance to have a result being printed, istribution.  Description Fragment of human Amino acid sequenc Amino acid sequenc Streptococcus poly propionibacterium Arabidopsis thalia Arabidopsis thalia Propionibacterium Arabidopsis thalia Propionibacterium Arabidopsis thalia Propionibacterium Arabidopsis an Arabidopsis thalia Propionibacterium M. tuberculosis an
OM protein Run on: Title: Scoring tal Searched: Word size Total numbo Maximum DB Maximum DB Post-proces and and score No. Score	GenCore versio Copyright (c) 1993 - 2003 - protein search, using sw model December 17, 2003, 14:50:14	US-10-045-180A-6 score: 31 table: 0LIGO Gapop 60.0 , Gapext 60.0 d: 1107863 seqs, 158726573 res ze : 0 DB seq length: 0 DB seq length: 0 DB seq length: 0	cessing: Listing first 100 summari:    A_Geneseq 19Jund3:*     SIDSIJ/gcgdata/geneseq 2:   SIDSIJ/gcgdata/geneseq 3:   SIDSIJ/gcgdata/geneseq 4:   SIDSIJ/gcgdata/geneseq 6:   SIDSIJ/gcgdata/geneseq 6:   SIDSIJ/gcgdata/geneseq 7:   SIDSIJ/gcgdata/geneseq 9:   SIDSIJ/gcgdata/geneseq 9:   SIDSIJ/gcgdata/geneseq 9:   SIDSIJ/gcgdata/geneseq 10:   SIDSIJ/gcgdata/geneseq 10:   SIDSIJ/gcgdata/geneseq 13:   SIDSIJ/gcgdata/geneseq 13:   SIDSIJ/gcgdata/geneseq 13:   SIDSIJ/gcgdata/geneseq 16:   SIDSIJ/gcgdata/geneseq 16:   SIDSIJ/gcgdata/geneseq 19:   SIDSIJ/gcgdata/geneseq 19:   SIDSIJ/gcgdata/geneseq 19:   SIDSIJ/gcgdata/geneseq 19:   SIDSIJ/gcgdata/geneseq 19:   SIDSIJ/gcgdata/geneseq 20:   SIDSIJ/gcgdata/geneseq 20:   SIDSIJ/gcgdata/geneseq 21:   SIDSIJ/gcgdata/geneseq 22:   SIDSIJ/gcgdata/geneseq 23:   SIDSIJ/gcgdata/geneseq 24:   SIDSIJ/gcgdata/genes	We. is the number of results predicted by greater than or equal to the score of the derived by analysis of the total score diagratured by analysis of the total score diagrams.  * SUMMARIES  Query  re Match Length DB ID  31 100.0 94 20 AAY01606  31 100.0 94 20 AAY01604  6 19.4 37 23 ABD26644  6 19.4 81 21 AAG59901  6 19.4 81 21 AAG59901  6 19.4 81 21 AAG59901  6 19.4 137 23 ABU57814  6 19.4 137 23 ABU57814

lung cancer or colorectal carcinoma, and for enhancing immunity, especially in the case of AIDS, or preventing immune deficiency, especially in the treatment of psoriasis, as well as for modulating inflammatory processes, especially in the case of chronic inflammatory

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Gaps

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ch 100.0%; Score 31; DB 20; Length 31; 1 Similarity 100.0%; Pred. No. 1.1e-24; 31; Conservative 0; Mismatches 0; Indels

Local Similarity

Matches

31 AA;

Sequence Query Match

disorders.

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1 ICHCRVLYCIFGEHLGGTCFILGERYPICCY 31 1 ICHCRVLYCIFGEHLGGTCFILGERYPICCY

Propionibacterium Propionibacterium	Propionibacterium Human immune/haema	Human ORFX protein	Propionibacterium	Human nervous syst	Human transcriptio	Propionibacterium	Human haematologic	Human haematologic	Human haematologic	Human haematologic	Human expressed pr	Human expressed pr	Human expressed pr	Human expressed pr	Propionibacterium
AAU52524 AAU57734	AAU40466 Aam82541	ABP04083	AAU50025	ABB16158	ABP35207	AAU46902	AAM80786	AAM81231	AAM81596	AAM81841	ABU04778	ABU04779	ABU04780	ABU04781	AAU46468
22	2 2	23	22	22	23	22	22	22	22	22	24	24	24	24	22
727	73	73	75	75	77	78	78	78	78	78	78	78	78	78	79
16.1	16.1	16.1	16.1	16.1	16.1	16.1	16.1	16.1	16.1	16.1	16.1	16.1	16.1	16.1	16.1
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8 8 4 4 4	85 86	87	88	89	90	91	95	93	94	95	96	97	86	66	100

## ALIGNMENTS

Human defensin; Def-X; antimicrobial; antiparasitic; pesticide; cytostatic; anticancer; inflammation; tissue repair; endocrine regulation; corticostatic regulation; cancer; melanoma;

AIDS; immune deficiency; psoriasis.

Homo sapiens FR2767832-A1. 05-MAR-1999 97FR-0010823. 97FR-0010823,

S.

(GEST ) GENSET 29-AUG-1997; 29-AUG-1997;

Amino acid sequence of the human defensin (Def-X) protein.

18-JUN-1999 (first entry)

AAY01603;

AAY01603 standard; protein; 94 AA.

RESULT 2 AAY01603

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Human defensin; Def-X; antimicrobial; antiparasitic; pesticide; cytostatic; anticancer; inflammation; tissue repair; endocrine regulation; corticostatic regulation; cancer; melanoma;
                                                                                                                                                                                                                                                                  Human defensin polypeptide Def-X - useful as antimicrobial agent,
                                                             Fragment of human defensin (Def-X) protein.
                                                                                              endocrine regulation; corticostatic AIDS; immune deficiency; psoriasis.
         AAY01606 standard; peptide; 31 AA.
                                                                                                                                                                                                                                                                          anticancer agent, pesticide, etc.
                                                                                                                                                                                                                                                                                            Claim 2; Page 33; 56pp; French.
                                                                                                                                                                             97FR-0010823.
                                                                                                                                                                                              97FR-0010823
                                                                                                                                                                                                                               Chumakov I;
                                           (first entry)
                                                                                                                                                                                                                                                 WPI; 1999-183266/16.
                                                                                                                                                                                                               SA.
                                                                                                                                                                                                              (GEST ) GENSET
                                                                                                                                                                                                                               Bougueleret L,
                                                                                                                                                                             29-AUG-1997;
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                                                                                                                         Homo sapiens
                                                                                                                                          FR2767832-A1
                                           18-JUN-1999
                           AAY01606;
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The present sequence represents human defensin (Def-X). The Def-X polypeptide can be used as an antimicrobial, antiparasitic agent or a pesticide. The Def-X polypeptide can be used as a cytostatic capt. The polypeptide can be used as a cytostatic for especially anticancer) agent, and as an agent for modulating processes of inflammation, tissue repair and endocrine (especially corticostatic) regulation. The polypeptide can be used in a composition for external topical use, especially in a cosmetic composition. Compositions and parasitic infections are dram-positive or -negative bacterial infections are associated with enveloped viruses, especially mere the viral infections are associated with enveloped viruses, especially melanomas, or liver cancer, prostate cancer, non-small-cell ung cancer or colorectal carcinoma, and for enhancing immunity, especially in the crastment of psoriasis, as well as for modulating infinantary in the treatment of psoriasis, as well as for modulating infinantory processes, especially in the case of AIDS, or prevention inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human defensin polypeptide Def-X - useful as antimicrobial agent,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anticancer agent, pesticide, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 1; 56pp; French.
                                                                                                                                                                                                                                                                                                                                                                                          Chumakov I;
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-183266/16.
                                                                                                                                                                                                                                                                                                                                                                                            Bougueleret L,
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The present sequence represents human defensin (Def-X) fragment. The Def-X polypeptide can be used as an antimicrobial, antiparasitic agent or a pesticide. The Def-X polypeptide can be used as a cytostatic (especially anticancer) agent, and as an agent for modulating processes of inflammation, tissue repair and endocrine (especially corticostatic) regulation. The polypeptide can be used in a composition for external copical use, especially in a cosmetic composition. Compositions or containing Def-X can be used for prevention and treatment of microbial and parasitic infections, especially where the microbial or parasitic infections are associated with enveloped viruses, or where the viral infections are associated with enveloped viruses, especially HSV and HIV. The compositions can used for prevention and/or treatment of cancers, especially melanomas, or liver cancer, prostate cancer, non-small-cell

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The present sequence represents human defensin (Def-X). The Def-X polypeptide can be used as an antimicrobial, antiparasitic agent or a pesticide. The Def-X polypeptide can be used as an offortatic agent or (sepecially anticancer) agent, and as an agent for modulating processes of inflammation, tissue repair and endocrine (especially corticostatic) regulation. The polypeptide can be used in composition for external topical use, especially in a cosmetic composition. Compositions containing Def-X can be used for prevention and treatment of microbial can parasitic infections, are Gram-positive or -negative bacterial infections or mycobacterial, fungal or spirochaete infections, or where the viral infections are associated with enveloped viruses, especially HSV and HIV. The compositions can used for prevention and/or treatment of cancers, especially melanomas, or liver cancer, prostate cancer, non-small-cell ung cancer or colorectal carcinoma, and for enhancing immunity, especially in the case of AIDS, or preventing immune deficiency, especially in the treatment of posciales, as well as for modulating inflammatory processes, especially in the case of AIDS.
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                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                     Human defensin; Def-X; antimicrobial; antiparasitic; pesticide; cytostatic; anticancer; inflammation; tissue repair; endocrine regulation; corticostatic regulation; cancer; melanoma; AIDS; immune deficiency; psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human defensin polypeptide Def-X - useful as antimicrobial agent,
                                                                   ö
                                 Length 94;
                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of the human defensin (Def-X) protein.
                             100.0%; Score 31; DB 20; Length 9
100.0%; Pred. No. 3e-24;
ive 0; Mismatches 0; Indels
                                                                                                                         64 ICHCRVLYCIFGEHLGGTCFILGERYPICCY 94
                                                                                                      1 ICHCRVLYCIFGEHLGGTCFILGERYPICCY 31
                                                                                                                                                                                                                             AAY01604 standard; protein; 94 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anticancer agent, pesticide, etc.
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                                                                                                                                                                                                                                                                                                 18-JUN-1999 (first entry)
                                                                  31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chumakov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-183266/16.
                                 Query Match
Best Local Similarity
94 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GEST ) GENSET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-MAR-1999
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                                                                                                                                                                                                                                                                AAY01604;
Sequence
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ch 100.0%; Score 31; DB 20; Length 94; l Similarity 100.0%; Pred. No. 3e-24; 31; Conservative 0; Mismatches 0; Indels

Query Match Best Local Similarity

Matches

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fire interiors. Street or a process. The interiors of street or street st
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                                                                                                                                                                                                                                                                                                                                                                               Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Streptococcus protein for the treatment or prevention of infectic or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a protein (ABP25413-ABP30895) from group B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fraser C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Telford J, Masignani V, Margarit Ros YI, Grandi G,
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100.0%; Pred. No. 39;
iive 0; Mismatches
                          64 ICHCRVLYCIFGEHLGGTCFILGERYPICCY
                                                                                                                                                                                                                                                                                                                                  Streptococcus polypeptide SEQ ID NO 2464.
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                                                                                                                                                                               ABP26644 standard; Protein; 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
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Matches 6; Conservative
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(GENO-) INST GENOMIC RES.
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                                       원
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                                                                                           RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cyquences Acoston Proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and ostecomyellitis), uveitis and endophthalmitis.

P. acnes is also involved in infections of bone, joints and the central rervous system, however it is particularly involved in the inflammatory lesions associated with acnes undertoned for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes infections. These antibodies can be used to diagnostic agents for determining P. acnes presence, for example, by charefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by consymptic captus for determining P. acnes presence, for example, by Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO C. at fip. wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                             SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endopthealmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
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                                                                                                                                                                                                                                                                                                                                                  Propionibacterium acnes immunogenic protein #19850.
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, Jen S,
                                                                                                                                                       AAU58954 standard; Protein; 64 AA.
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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L'maisonneuve J, Zhang Y,
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Best Local Similarity 100.
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   ILGERY 12
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N-PSDB; AAS59596.
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                        Arabidopsis thaliana protein fragment SEQ ID NO: 77532.
AAG59901 standard; Protein; 81 AA.
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99US-01342863.
99US-0134218.
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                                                                                  Arabidopsis thaliana
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Scoring table:

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Sequence 311, App Sequence 311, App Sequence 311, App Sequence 150, App Sequence 150, App Sequence 190, App Sequence 235, App Sequence 231, App Sequence 234, App Sequence 235, App Sequence 235
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 Sequence 6, Appli
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Sequence 351, Appl
Sequence 351, Appl
Sequence 11204, A
Sequence 11204, A
Sequence 118, Appl
Sequence 114, Appl
Sequence 114, Appl
Sequence 114, Appl
Sequence 115, Appl
Sequence 271, Appl
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466.897 Million cell updates/sec
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                 GenCore version 5.1.6
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| US-10-080-170-351
| US-09-864-761-37998
| US-09-813-453A-61
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| US-09-913-453A-61
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and is derived by analysis of
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Sequence 6, Appli
Sequence 8, Appli
Sequence 11, Appli
Sequence 62, Appli
Sequence 62, Appli
Sequence 61, Appli
Sequence 21, Appli
Sequence 21, Appli
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 Sequence 2, Appl:
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Publication No. US20020115151A1
GENERAL INFORMATION:
APPLICANT: GENSET SA
TITLE OF INVENTION: HUMAN DEFENSIN DEF-X GENE AND DNAC
COMPOSITION CONTAINING SAME AND DIAGNOSTIC AND THERAPBUTIC APPLICATIONS
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ZIP: 92101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: PATENTIN FO-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/013,770
FILLING DATA:
APPLICATION NUMBER: 09/486,580
FILLING DATE: CUNKNOWN->
ATTORNEY/AGENT INFORMATION:
MAME: HART, DAMIE: 40,637
REFERENCE/DOCKET NUMBER: GENSET.064CI
; INFORMATION FOR REQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; SEQUENCE CHARACTERISTICS:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 AMINO ACIDS
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US-10-188-947-3
US-10-080-170-21
US-10-156-761-13747
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STREET: 550 West C Street
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100.0%; Score 31; DB 14;
Best Local Similarity 100.0%; Pred. No. 2.3e-25;
Matches 31; Conservative 0; Mismatches 0;
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US-09-750-963-8
US-09-902-773A-9
US-09-425-021-11
US-09-995-598-62
US-09-995-598-62
US-10-189-60-12
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SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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US-10-045-180A-6
; Sequence 6, Application US/10045180A
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CORRESPONDENCE ADDRESS:
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STATE: California
COUNTRY: USA
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RESULT 1
US-10-013-770-6
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GENERAL INFORMATION:

APPLICANT: Bougueleret, Lydie
APPLICANT: Bougueleret, Lydie
APPLICANT: Chumakov, Ilya
ITILE OF INVENTION: Containing Them and Applications to Diagnosis and to Therapeuti
ITILE OF INVENTION: Containing Them and Applications to Diagnosis and to Therapeuti
ITILE OF INVENTION: CONTAINING THEM SEPERANCE: GEN-1001
CURRENT APPLICATION NUMBER: US/10/045,180A
CURRENT FILING DATE: 2001-10-18
FRIOR PELING DATE: 1998-08-28
PRIOR PELING DATE: 1998-08-28
PRIOR APPLICATION NUMBER: FF7/FF89/01864
PRIOR APPLICATION NUMBER: FF 97/10823
PRIOR FILING DATE: 1997-08-29
PRIOR FILING DATE: 1997-08-29
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
SEQ ID NO 6
SEC ID NO 6
SERVICE THE SEQ ID NOS: 12
SEX ID NO 6
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US-10-013-770-3
US-10-013-770-3

US-10-013-770-3

Sequence 3, Application US/10013770

Publication No. US20020115151A1

GENERAL INFORMATION:

APPLICANT: GENERT SA

TITLE OF INVENTION: HUMAN DEFENSIN DEF-X GENE AND DNAC

COMPOSITION CONTAINING SAME AND DIAGNOSTIC AND

THERAPEUTIC APPLICATIONS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/013,770
FILING DATE: 10-Dec-2001
PRIOR APPLICATION DATA:
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ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 550 West C Street
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100.0%; Pred. No. 2.3e-25;
tive 0; Mismatches 0;
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REGISTRATION NUMBER: 40,637
REFERENCE/DOCKET NUMBER: GENSET.064C1
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 94 AMINO ACIDS
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FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(31)
OTHER INFORMATION: Def-X mature peptide
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STRANDEDNESS: SINGLE
Publication No. US20020182703A1
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STATE: California
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ORGANISM: Homo sapiens
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188.888 Million cell updates/sec
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seq length: 200000000
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                                                                                                                                                                                                                                      Title:
Perfect score:
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                                                                                                          OM protein
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                                                                                                                                                                                                                                                                                Sequence:
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Patent No. 6329340

GENERAL INFORMATION:
APPLICANT: GENEST SA

TITLE OF INVENTION: HUMAN DEFENSIN DEF-X GENE AND DNAC

TITLE OF INVENTION: THERAPEUTIC APPLICATIONS

NUMBER OF SEQUENCES: 6

CORRESPONDENCE S:
ADDRESSE: Knobbe, Martens, Olson & Bear

STREE: S50 West C Street

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92101
                                                                                                                                                                                 Sequence 6, Application US/09486580A;
Sequence 6, Application US/09486580A;
Patent No. 6329340

GENERAL INFORMATION:
APPLICANT: GENSET SA
TITLE OF INVENTION: COMPOSITION CONTAINING SAME AND DNAC;
TITLE OF INVENTION: THERAPEUTIC APPLICATIONS
INTHER OF SEQUENCES;
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 550 West C Street
STREET: 550 West C Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USERIA COUNTRY: USERIA: USERI
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ALIGNMENTS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 100.0
MATChes 31; Conservative
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STATE: California
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US-09-486-580A-3
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US-09-486-580A-6
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Sequence 5707, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
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                                 CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/486,580A

FILING DATE: FEBRUARY 25, 2000

ATTORNEY/AGENT INFORMATION:

NAME: Hart, Daniel

REGISTRATION NUMBER: 40,637

FREFERENCE/DOCKET NUMBER: GENSET.064C1

SEQUENCE CHARACTERISTICS:

LENGTH: 94 AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 31; DB 4; Length 94; 100.0%; Pred. No. 3e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: PC
COMPUTER: PC
COMPAND
SYSTEM: «Unknown»
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
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Best Local Similarity 100.0%; Pred. No. 3e-Matches 31; Conservative 0; Mismatches
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REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMĀTION:
NAME: Ariniello, Pamela Deneke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION UMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
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COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                         TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLLOGY: LINEAR
MOLECULE TYPE: PROTEIN
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
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64..94
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US-09-107-532A-5707
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LOCATION:
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PEATURE:
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